STIC-Biotech/ChemLib 135891

From: Swope, Sheridan
Sent: Friday, October 22, 2004 3:41 PM
To: STIC-Biotech/ChemLib
Cc: Schreiber, David
Subject: 09/980,881

Please forward to David Schreiber

David,

For 09/980,881,

pls search and interference search:
SID 9 against the NT and AA data bases, wherein the maximum length of the polypeptide hit is 19 amino acids and the maximum length of the polynucleotide hit is 57 nucleotides.

pls interference search only:
SID 1, residues 18-1097, against the NT and AA data bases
SID 2 full-length regular and oligo against the NT and AA data bases
SID 3 full-length regular and oligo against the NT and AA data bases
SID 4 full-length regular and oligo against the NT and AA data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

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Peggy Ruppel

****
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Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 00:07:08 ; Search time 380 Seconds
(without alignments)
193.400 Million cell updates/sec

Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 4074946

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09980881/runat_28102004_131502_11391/app_query.fasta_1.199
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57
-USER=US09980881_@CGN_1_1_470_@runat_28102004_131502_11391 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	46	65.7	43	4	AAF80298	Aaf80298 PCR prime
c	2	37	52.9	41	6	ABZ48454	Abz48454 Human org
	3	37	52.9	51	2	AAT00624	Aat00624 Human (2'
	4	36	51.4	36	10	ADD69569	Add69569 Food enri
c	5	36	51.4	36	10	ADD69568	Add69568 Food enri
	6	36	51.4	51	4	AAL27400	Aal27400 Human SNP
	7	35.5	50.7	39	2	AAQ36595	Aaq36595 PCR prime
c	8	35	50.0	45	2	AAZ33905	Aaz33905 Human PRO
c	9	35	50.0	45	3	AAC78611	Aac78611 Human PRO
c	10	35	50.0	45	6	ABK40321	Abk40321 Oligonucl
c	11	35	50.0	45	8	ACA63473	Aca63473 Novel hum
c	12	35	50.0	45	8	ACA71637	Aca71637 Human PRO
c	13	35	50.0	45	8	ABX92277	Abx92277 Human PRO
c	14	35	50.0	45	8	ACA66018	Aca66018 Human sec
c	15	35	50.0	45	9	ADA24556	Ada24556 Secreted
c	16	35	50.0	45	9	ACD29619	Acd29619 Novel hum
c	17	35	50.0	45	9	ADA12217	Ada12217 Human sec
c	18	35	50.0	45	9	ACD29034	Acd29034 Novel hum
c	19	35	50.0	45	10	ADB73523	Adb73523 Human PRO
c	20	35	50.0	45	10	ADB76239	Adb76239 Human PRO
c	21	35	50.0	45	10	ADC43665	Adc43665 Human PRO
c	22	35	50.0	45	10	ADC61425	Adc61425 Human PRO
c	23	35	50.0	45	10	ADC63389	Adc63389 Human PRO
c	24	35	50.0	45	10	ADC66489	Adc66489 Human PRO
c	25	35	50.0	45	10	ADC68613	Adc68613 Human PRO
c	26	35	50.0	45	10	ADC62673	Adc62673 Human PRO
c	27	35	50.0	45	10	ADC67738	Adc67738 Human PRO
c	28	35	50.0	45	10	ADC41058	Adc41058 Human PRO
c	29	35	50.0	45	10	ADC67113	Adc67113 Human PRO
c	30	35	50.0	45	10	ADC62049	Adc62049 Human PRO
c	31	35	50.0	45	10	ADC41682	Adc41682 Human PRO
c	32	35	50.0	45	10	ADE49051	Ade49051 Human PRO
c	33	35	50.0	45	10	ADE35105	Ade35105 Human PRO
c	34	35	50.0	45	10	ADE16219	Ade16219 Human PRO
c	35	35	50.0	45	10	ADD72834	Add72834 Human PRO
c	36	35	50.0	45	10	ADD72192	Add72192 Human PRO
c	37	35	50.0	45	10	ADE16843	Ade16843 Human PRO
c	38	35	50.0	45	10	ADF46857	Adf46857 Human PRO
c	39	35	50.0	45	10	ADG52614	Adg52614 Human PRO
c	40	35	50.0	45	10	ADG59934	Adg59934 Human PRO
c	41	35	50.0	45	10	ADI60694	Adi60694 Human PRO
c	42	35	50.0	45	10	ADJ37384	Adj37384 Tumour th
c	43	35	50.0	45	10	ACD42438	Acd42438 Novel hum
c	44	35	50.0	45	12	ADE48351	Ade48351 Human PRO
c	45	35	50.0	45	12	ADE89452	Ade89452 Human PRO

ALIGNMENTS

RESULT 1
AAF80298/c
ID AAF80298 standard; DNA; 43 BP.
XX
AC AAF80298;
XX
DT 29-JUN-2001 (first entry)
XX
DE PCR primer used to amplify the RK2 origin of replication.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant;
KW PCR primer; ss.
XX
OS Escherichia coli.
XX
PN FR2798139-A1.
XX
PD 09-MAR-2001.
XX
PF 03-SEP-1999; 99FR-00011112.
XX
PR 03-SEP-1999; 99FR-00011112.
XX
PA (MERI-) MERISTEM THERAPEUTICS SA.
XX
PI Gruber V, Comeau D;
XX
DR WPI; 2001-259847/27.
XX

PT New vector free from non-essential elements, useful for transforming
PT cells for protein production and for preparing transgenic plants.
XX
PS Example 1; Page 13; 180pp; French.
XX
CC The specification describes a synthetic vector containing only those
CC elements essential for its functionality and transgenesis of a cell
CC (especially a plant cell). The vector consists of at most one origin of
CC replication (ori), at most one sequence encoding a selection agent and a
CC trfA locus encoding a protein that increases the level of plasmid
CC replication. The vector particularly contains an RK2 ori, especially oriV
CC from pRK2 of Escherichia coli with a broad host range, an antibiotic
CC resistance gene (especially nptIII conferring resistance to kanamycin in
CC bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
CC The vectors are used to prepare transgenic plants and transformed host
CC cells for production of a heterologous proteins, e.g. insulin,
CC interferon, lipase, blood proteins and anti-inflammatory agents. PCR
CC primers AAF80297-98 were used to amplify the RK2 ori, and the amplified
CC fragment was used to construct plasmids of the invention
XX
SQ Sequence 43 BP; 11 A; 6 C; 17 G; 9 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.67	Length:	43
Score:	46.00	Matches:	9
Percent Similarity:	90.91%	Conservative:	1
Best Local Similarity:	81.82%	Mismatches:	1
Query Match:	65.71%	Indels:	0
DB:	4	Gaps:	0

US-09-980-881A-9 (1-14) x AAF80298 (1-43)

```
Qy          1 SerAsnProProValGluLysLeuLeuProLeu 11
              ||||||||||||||:::   ||||||||||||
Db         38 TCGAACCCTCCCGTGAAAGGCCTTCTACCATTA 6
```

RESULT 2
ABZ48454/c
ID ABZ48454 standard; DNA; 41 BP.
XX
AC ABZ48454;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human organic cation transporter OCT1 gene polymorphic site, #5237.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KW drug evaluation; drug screening; genotyping; genetic profiling;
KW therapeutic customisation; adverse reaction; clinical trial;
KW drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-JP011592.
XX
PR 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
PA (RIKE) RIKEN KK.
XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX
DR WPI; 2002-583571/62.
XX
PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
PS Claim 23; Page 166; 2785pp; English.
XX
CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to a an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 11 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	276	Length:	41
Score:	37.00	Matches:	7
Percent Similarity:	77.78%	Conservative:	0
Best Local Similarity:	77.78%	Mismatches:	2
Query Match:	52.86%	Indels:	0
DB:	6	Gaps:	0

US-09-980-881A-9 (1-14) x ABZ48454 (1-41)

```
Qy          3 ProProValGluLysLeuLeuProLeu 11
              ||||||||||||       |||||||||
Db         33 CCACCTGTGGAGCCTTTCCTACCACTG 7
```

RESULT 3
AAT00624
ID AAT00624 standard; DNA; 51 BP.
XX
AC AAT00624;
XX
DT 03-FEB-1996 (first entry)
XX
DE Human (2'-5') oligo A synthetase antigenic peptide cDNA.
XX
KW (2'-5') oligo A synthetase; interferon; antigenic peptide; ss.
XX
OS Homo sapiens.
XX
PN CA1337281-C.

XX
PD 10-OCT-1995.
XX
PF 18-APR-1985; 85CA-00479458.
XX
PR 18-APR-1984; 84US-00601782.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Revel M, Chebath J;
XX
DR WPI; 1995-366737/48.
DR P-PSDB; AAR84190.
XX
PT New DNA encoding 2'-5' oligo A synthetase and related vectors -
PT transformed microorganisms, proteins and antigenic peptide(s), useful for
PT monitoring interferon activity in cells and body fluids.
XX
PS Claim 7; Fig 7a; 75pp; English.
XX
CC Enzyme AAR84186 has a mol.wt. of about 41,500 daltons. AA sequence
CC AAR84186 is claimed. Also claimed is the antigenic peptide AAR84190 which
CC is AAs 348-364 of AAR84186. A DNA molecule coding for a C-terminal
CC heptadecapeptide of (2'-5') oligo A synthetase comprising nts 1075-1124
CC of AAT00619 is claimed. This encodes AAR84190, and its sequence is given
CC in AAT00624. For further information see AAR84186 and AAT00619
XX
SQ Sequence 51 BP; 7 A; 24 C; 6 G; 14 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	355	Length:	51
Score:	37.00	Matches:	7
Percent Similarity:	66.67%	Conservative:	1
Best Local Similarity:	58.33%	Mismatches:	4
Query Match:	52.86%	Indels:	0
DB:	2	Gaps:	0

US-09-980-881A-9 (1-14) x AAT00624 (1-51)

```
Qy          3 ProProValGluLysLeuLeuProLeuSerLeuLys 14
              ||||||           ||||||||||:::|||
Db         14 CCTCCCTGCCATTCATCCCTGCCCCTCTCCATGAAG 49
```

RESULT 4
ADD69569
ID ADD69569 standard; DNA; 36 BP.
XX
AC ADD69569;
XX
DT 15-JAN-2004 (first entry)
XX
DE Food enrichment-related PCR primer QCR1 - SEQ ID 49.
XX
KW food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;
KW PCR; primer; ss; QCR1.
XX
OS Unidentified.
XX
PN WO2003080832-A1.
XX
PD 02-OCT-2003.
XX
PF 26-MAR-2003; 2003WO-JP003715.
XX
PR 26-MAR-2002; 2002JP-00085058.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Nishiuchi H, Nishimura Y, Kuroda M;
XX
DR WPI; 2003-833508/77.
XX
PT Genetically-modified Candida utilis for producing foods and drinks
PT enriched with gamma-glutamyl cysteine or cysteine, useful in food
PT industry e.g. for seasoning, by culturing and processing to enhance
PT flavor.
XX
PS Example 3; SEQ ID NO 49; 70pp; Japanese.
XX
CC The invention relates to a novel method for producing a food containing
CC gamma-glutamyl cysteine or cysteine comprising culturing under
CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or
CC more by weight of gamma-glutamyl cysteine based on dry cells in the
CC logarithmic growth phase when cultured in the minimum medium, adding the
CC obtained culture, optionally after heating, to a food or drink material
CC and processing. The yeast of the invention may be used for producing food
CC and drink with enriched gamma-glutamyl cysteine or cysteine which is
CC useful in food industry e.g. for seasoning. In this way, food and drink
CC can be cheaply produced with improved flavour. The current sequence is
CC that of the food enrichment-related PCR primer of the invention.
XX
SQ Sequence 36 BP; 16 A; 9 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	352	Length:	36
Score:	36.00	Matches:	7
Percent Similarity:	72.73%	Conservative:	1
Best Local Similarity:	63.64%	Mismatches:	3
Query Match:	51.43%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x ADD69569 (1-36)

```
Qy          4 ProValGluLysLeuLeuProLeuSerLeuLys 14
              |||:::|||||||||||||||          |||
Db          4 CCTATTGAAAAATTACTACCCACCCAAGAAAAG 36
```

RESULT 5
ADD69568/c
ID ADD69568 standard; DNA; 36 BP.
XX
AC ADD69568;
XX
DT 15-JAN-2004 (first entry)
XX
DE Food enrichment-related PCR primer QCF1 - SEQ ID 48.
XX
KW food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;
KW PCR; primer; ss; QCF1.
XX
OS Unidentified.
XX
PN WO2003080832-A1.
XX
PD 02-OCT-2003.
XX
PF 26-MAR-2003; 2003WO-JP003715.
XX
PR 26-MAR-2002; 2002JP-00085058.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Nishiuchi H, Nishimura Y, Kuroda M;
XX
DR WPI; 2003-833508/77.
XX
PT Genetically-modified Candida utilis for producing foods and drinks
PT enriched with gamma-glutamyl cysteine or cysteine, useful in food
PT industry e.g. for seasoning, by culturing and processing to enhance
PT flavor.
XX
PS Example 3; SEQ ID NO 48; 70pp; Japanese.
XX
CC The invention relates to a novel method for producing a food containing
CC gamma-glutamyl cysteine or cysteine comprising culturing under
CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or

CC more by weight of gamma-glutamyl cysteine based on dry cells in the
CC logarithmic growth phase when cultured in the minimum medium, adding the
CC obtained culture, optionally after heating, to a food or drink material
CC and processing. The yeast of the invention may be used for producing food
CC and drink with enriched gamma-glutamyl cysteine or cysteine which is
CC useful in food industry e.g. for seasoning. In this way, food and drink
CC can be cheaply produced with improved flavour. The current sequence is
CC that of the food enrichment-related PCR primer of the invention.
XX
SQ Sequence 36 BP; 7 A; 4 C; 9 G; 16 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	352	Length:	36
Score:	36.00	Matches:	7
Percent Similarity:	72.73%	Conservative:	1
Best Local Similarity:	63.64%	Mismatches:	3
Query Match:	51.43%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x ADD69568 (1-36)

```
Qy          4 ProValGluLysLeuLeuProLeuSerLeuLys 14
              |||:::|||||||||||||||        |||
Db         33 CCTATTGAAAAATTACTACCCACCCAAGAAAAG 1
```

RESULT 6
AAL27400
ID AAL27400 standard; DNA; 51 BP.
XX
AC AAL27400;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #608.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 1561; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 11 A; 18 C; 9 G; 13 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	525	Length:	51
Score:	36.00	Matches:	7
Percent Similarity:	76.92%	Conservative:	3
Best Local Similarity:	53.85%	Mismatches:	3
Query Match:	51.43%	Indels:	0
DB:	4	Gaps:	0

US-09-980-881A-9 (1-14) x AAL27400 (1-51)

```
Qy          1 SerAsnProProValGluLysLeuLeuProLeuSerLeu 13
              |||   |||||||||   :::   ||||||:::::|||
Db          1 AGCAGGCCTCCTGTAGCTCGCTAATTACCCGTGACTTTA 39
```

RESULT 7
AAQ36595
ID AAQ36595 standard; DNA; 39 BP.
XX
AC AAQ36595;
XX
DT 25-MAR-2003 (revised)
DT 28-MAY-1993 (first entry)
XX
DE PCR primer FH for construction of humanised Heavy chain anti IL-2 Ab.
XX
KW antibody; monoclonal; chimaeric; grafted; humanised; IL-2; interleukin-2;
KW cytokines; interleukin-2 receptor; 55kD beta chain; activated T cells;
KW T cell mediated disease; graft versus host disease; transplant rejection;
KW autoimmune diseases; chemotherapy; immunosuppressants; T cell typing;
KW diagnosis; testing; detection; ss.
XX
OS Synthetic.
XX
PN WO9301289-A1.
XX
PD 21-JAN-1993.
XX
PF 10-JUL-1992; 92WO-GB001258.
XX
PR 11-JUL-1991; 91GB-00015010.
XX
PA (WELL) WELLCOME FOUND LTD.
PA (WALD/) WALDMANN H.
XX
PI Waldmann H, Winter GP, Crowe JS, Lewis AP;
XX
DR WPI; 1993-045493/05.
XX
PT Human interleukin-2 receptor antibodies - useful for treating and
PT preventing T-cell mediated diseases e.g. graft versus host disease,
PT transplant rejection etc.
XX
PS Example; Page 42; 48pp; English.
XX
CC This PCR primer was used with AAQ36594 in the construction of a humanised
CC anti-IL-2 antibody. The initial template for the reaction was anti-CD4
CC heavy chain (on KOL framework; WO9205274). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 39 BP; 11 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:              469          Length:        39
Score:                  35.50        Matches:       9
Percent Similarity:     83.33%       Conservative:  1
Best Local Similarity:  75.00%       Mismatches:    1
Query Match:            50.71%       Indels:        1
DB:                     2            Gaps:          1

US-09-980-881A-9 (1-14) x AAQ36595 (1-39)

Qy          3 ProProValGluLysLeuLeuProLeuSerLeuLys 14
              |||||||||   ||||||||||||||:::   |||
Db          5 CCCCCGGTG---AAGCTGCTACCTCTTGCACAGAAA 37

RESULT 8
AAZ33905/c
ID   AAZ33905 standard; DNA; 45 BP.
XX
AC   AAZ33905;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human PRO274 hybridisation probe.
XX
KW   Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW   probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW   secreted protein; transmembrane protein; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9946281-A2.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US005028.
XX
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   31-MAR-1998;   98US-0080105P.
PR   31-MAR-1998;   98US-0080107P.
PR   31-MAR-1998;   98US-0080165P.
PR   31-MAR-1998;   98US-0080194P.
PR   01-APR-1998;   98US-0080327P.
PR   01-APR-1998;   98US-0080328P.
PR   01-APR-1998;   98US-0080333P.
PR   01-APR-1998;   98US-0080334P.
PR   08-APR-1998;   98US-0081049P.
PR   08-APR-1998;   98US-0081070P.
PR   08-APR-1998;   98US-0081071P.
PR   09-APR-1998;   98US-0081195P.
PR   09-APR-1998;   98US-0081203P.
PR   09-APR-1998;   98US-0081229P.
PR   15-APR-1998;   98US-0081817P.
PR   15-APR-1998;   98US-0081838P.
PR   15-APR-1998;   98US-0081952P.
PR   15-APR-1998;   98US-0081955P.
PR   21-APR-1998;   98US-0082568P.
PR   21-APR-1998;   98US-0082569P.
PR   22-APR-1998;   98US-0082700P.
PR   22-APR-1998;   98US-0082704P.
PR   22-APR-1998;   98US-0082804P.
PR   23-APR-1998;   98US-0082767P.
PR   23-APR-1998;   98US-0082796P.
PR   27-APR-1998;   98US-0083336P.
PR   28-APR-1998;   98US-0083322P.
PR   29-APR-1998;   98US-0083392P.
PR   29-APR-1998;   98US-0083495P.
PR   29-APR-1998;   98US-0083496P.
PR   29-APR-1998;   98US-0083499P.
PR   29-APR-1998;   98US-0083500P.
PR   29-APR-1998;   98US-0083545P.
PR   29-APR-1998;   98US-0083554P.
PR   29-APR-1998;   98US-0083558P.
PR   29-APR-1998;   98US-0083559P.
PR   30-APR-1998;   98US-0083742P.
PR   05-MAY-1998;   98US-0084366P.
PR   06-MAY-1998;   98US-0084414P.
PR   06-MAY-1998;   98US-0084441P.
PR   07-MAY-1998;   98US-0084598P.
PR   07-MAY-1998;   98US-0084600P.
PR   07-MAY-1998;   98US-0084627P.
PR   07-MAY-1998;   98US-0084637P.
PR   07-MAY-1998;   98US-0084639P.
PR   07-MAY-1998;   98US-0084640P.
PR   07-MAY-1998;   98US-0084643P.
PR   13-MAY-1998;   98US-0085323P.
PR   13-MAY-1998;   98US-0085338P.
PR   13-MAY-1998;   98US-0085339P.
PR   15-MAY-1998;   98US-0085573P.
PR   15-MAY-1998;   98US-0085579P.
PR   15-MAY-1998;   98US-0085580P.
PR   15-MAY-1998;   98US-0085582P.
PR   15-MAY-1998;   98US-0085689P.
PR   15-MAY-1998;   98US-0085697P.
PR   15-MAY-1998;   98US-0085700P.
PR   15-MAY-1998;   98US-0085704P.
PR   18-MAY-1998;   98US-0086023P.
PR   22-MAY-1998;   98US-0086392P.
PR   22-MAY-1998;   98US-0086414P.
PR   22-MAY-1998;   98US-0086430P.
PR   22-MAY-1998;   98US-0086486P.
PR   28-MAY-1998;   98US-0087098P.
PR   28-MAY-1998;   98US-0087106P.
PR   28-MAY-1998;   98US-0087208P.
PR   30-JUL-1998;   98US-0094651P.
PR   11-SEP-1998;   98US-0100038P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wood WI,  Goddard A,  Gurney A,  Yuan J,  Baker KP,  Chen J;
XX
DR   WPI; 1999-551358/46.
XX
PT   New secreted and transmembrane polypeptides and their polynucleotides,
PT   useful for treating blood coagulation disorders, cancers and cellular
PT   adhesion disorders.
XX
PS   Example 4; Page 184; 530pp; English.
XX
CC   The present invention describes secreted and transmembrane polypeptides
CC   and their polynucleotides. The nucleotide sequences are useful as sources
CC   of probes, primers, for chromosome mapping, and for generation of
CC   antisense sequences. They can also be used to create transgenic animals.
CC   The proteins can be used to treat a variety of diseases and disorders,
CC   depending on their function. Diseases that may be treated include blood
CC   coagulation disorders, cancers and cellular adhesion disorders. They may
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CC   also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC   AAY41774 represent polynucleotide and polypeptide sequence given in the
CC   exemplification of the present invention
XX
SQ   Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              672          Length:        45
Score:                  35.00        Matches:       7
Percent Similarity:     80.00%       Conservative:  1
Best Local Similarity:  70.00%       Mismatches:    2
Query Match:            50.00%       Indels:        0
DB:                     2            Gaps:          0

US-09-980-881A-9 (1-14) x AAZ33905 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 9
AAC78611/c
ID   AAC78611 standard; DNA; 45 BP.
XX
AC   AAC78611;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human PRO274 hybridisation probe SEQ ID NO:17.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW   expressed sequence tag; detection; cancer; PCR primer; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200053756-A2.
XX
PD   14-SEP-2000.
XX
PF   18-FEB-2000; 2000WO-US004341.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   29-MAR-1999;   99US-0126773P.
PR   21-APR-1999;   99US-0130232P.
PR   28-APR-1999;   99US-0131445P.
PR   14-MAY-1999;   99US-0134287P.
PR   23-JUN-1999;   99US-0141037P.
PR   26-JUL-1999;   99US-0145698P.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-611443/58.
XX
PT   Novel PRO polypeptides and polynucleotides used in detection methods, to
PT   target bioactive molecules to specific cells, and to modulate cellular
PT   activities.
XX
PS   Example 4; Page 235; 636pp; English.
XX
CC   AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC   tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC   The PRO polynucleotides and polypeptides have cytostatic activity. The
CC   polynucleotides and polypeptides can be used for detecting the presence
CC   of PRO polypeptides in samples, for linking bioactive molecules to cells
CC   and for modulating biological activities of cells, using the polypeptides
CC   for specific targeting. The polypeptide targeting can be used to kill the
CC   target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC   provide specific targeting of bioactive molecules to cells. AAC78600 to
CC   AAC78987 represent PCR primers and probes used in the isolation of the
CC   PRO polynucleotide sequences
XX
SQ   Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              672          Length:        45
Score:                  35.00        Matches:       7
Percent Similarity:     80.00%       Conservative:  1
Best Local Similarity:  70.00%       Mismatches:    2
Query Match:            50.00%       Indels:        0
DB:                     3            Gaps:          0

US-09-980-881A-9 (1-14) x AAC78611 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 10
ABK40321/c
ID   ABK40321 standard; DNA; 45 BP.
XX
AC   ABK40321;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Oligonucleotide probe for human PRO274 DNA.
XX
KW   Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW   leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW   neuroprotective; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153486-A1.
XX
PD   26-JUL-2001.
XX
PF   11-FEB-2000; 2000WO-US003565.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   11-MAR-1999;   99US-0123972P.
PR   11-MAY-1999;   99US-0133459P.
PR   02-JUN-1999;   99WO-US012252.
PR   22-JUN-1999;   99US-0140650P.
PR   22-JUN-1999;   99US-0140653P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149395P.
PR   31-AUG-1999;   99US-0151689P.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   05-JAN-2000; 2000WO-US000219.
XX
PA   (GETH ) GENENTECH INC.
```

XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
PS Example 10; Page 120; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC antibodies are useful for treating benign or malignant tumours (e.g.
CC renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC malignancies, other disorders such as neuronal, glial, astrocytal,
CC hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders,
CC inflammatory, immune and angiogenic disorders. The polynucleotide
CC sequences are also useful in gene therapy. The present sequence
CC represents a probe used in the methods of the present invention
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	6	Gaps:	0

US-09-980-881A-9 (1-14) x ABK40321 (1-45)

```
Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
```

RESULT 11
ACA63473/c
ID ACA63473 standard; DNA; 45 BP.
XX
AC ACA63473;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein related probe #2.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; probe; ss.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328860/31.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Example 4; Page 125; 453pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence represents a novel human secreted and
CC transmembrane PRO polypeptide associated probe
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	8	Gaps:	0

US-09-980-881A-9 (1-14) x ACA63473 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
```

RESULT 12
ACA71637/c
ID ACA71637 standard; DNA; 45 BP.
XX
AC ACA71637;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 17.
XX
KW Human; ds; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328499/31.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
PS Disclosure; SEQ ID NO 17; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preeclampsia; carcinogenesis. The present sequence represents a PRO
CC polypeptide associated oligonucleotide of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	8	Gaps:	0

US-09-980-881A-9 (1-14) x ACA71637 (1-45)

```
Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
```

RESULT 13
ABX92277/c
ID ABX92277 standard; DNA; 45 BP.
XX
AC ABX92277;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO DNA probe SEQ ID No 17.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant; probe; ss.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-00978697.
XX
PR 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.

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PR   10-MAR-1999;   99WO-US005190.
PR   12-APR-1999;   99US-00284291.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380142.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000US-00709238.
PR   27-NOV-2000; 2000US-00723749.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   22-MAR-2001; 2001US-00816920.
PR   22-MAR-2001; 2001WO-US009552.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi A,  Baker KP,  Botstein D,  Desnoyers L,  Eaton D;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-288163/28.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides
PT   encoding them useful for treating cancer, kidney diseases, bone,
PT   cartilage disorders and immune deficiencies.
XX
PS   Example 4; Page 126; 459pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for linking
CC   bioactive molecules to cells expressing PRO polypeptides, for modulating
CC   biological activities of cells expressing PRO polypeptides, and for for
CC   identifying agonists or antagonists. The bioactive molecule maybe a
CC   toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC   The PRO polypeptides are useful for treating immune disorders, diabetes
CC   or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC   disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC   tumours, and wound healing. The polynucleotide sequences encoding PRO
CC   polypeptides are useful as hybridisation probes, in chromosome and gene
CC   mapping, in the generation of antisense RNA and DNA, in the preparation
CC   of PRO polypeptides, for generating transgenic animals or knockout
CC   animals, for the genetic analysis of individuals with genetic disorders,
CC   and in gene therapy. The present sequence represents a probe used in the
CC   examples of the present invention. Note: The sequence data for this
CC   patent was obtained in electronic format directly from the USPTO web site
CC   at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                672             Length:          45
Score:                    35.00           Matches:         7
Percent Similarity:       80.00%          Conservative:    1
Best Local Similarity:    70.00%          Mismatches:      2
Query Match:              50.00%          Indels:          0
DB:                       8               Gaps:            0

US-09-980-881A-9 (1-14) x ABX92277 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 14
ACA66018/c
ID   ACA66018 standard; DNA; 45 BP.
XX
AC   ACA66018;
XX
DT   24-JUN-2003  (first entry)
XX
DE   Human secreted/transmembrane protein PRO274 probe.
XX
KW   Human; ss; secreted protein; transmembrane protein; PRO; probe;
KW   malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW   leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW   infertility; premature aging; psoriasis; inflammatory disease;
KW   renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW   hepatitis; multiple sclerosis; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003004102-A1.
XX
PD   02-JAN-2003.
XX
PF   15-OCT-2001; 2001US-00978189.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
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PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-341189/32.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
PS Example 4; Page 121; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence is a probe used in the isolation of a cDNA
CC encoding a PRO polypeptide
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	8	Gaps:	0

US-09-980-881A-9 (1-14) x ACA66018 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
```

RESULT 15
ADA24556/c
ID ADA24556 standard; DNA; 45 BP.
XX
AC ADA24556;

XX
DT 20-NOV-2003 (first entry)
XX
DE Secreted and transmembrane PRO protein associated probe #2.
XX
KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder; probe; ss.
XX
OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
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PR 28-MAY-1998; 98US-0087208P.
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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-521814/49.
XX
PT New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
PS Example 4; Page 132; 461pp; English.
XX
CC The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
CC polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for

Alignment Scores:

Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	9	Gaps:	0

US-09-980-881A-9 (1-14) x ADA24556 (1-45)

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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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Search completed: October 31, 2004, 02:18:06
Job time : 386 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 19:21:49 ; Search time 38 Seconds
(without alignments)
24.433 Million cell updates/sec

Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 179518

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	35	50.0	17	2	US-08-964-725-15	Sequence 15, Appl
2	33	47.1	12	4	US-09-007-288E-88	Sequence 88, Appl
3	30	42.9	14	3	US-09-400-653A-31	Sequence 31, Appl
4	30	42.9	14	3	US-09-248-061B-27	Sequence 27, Appl
5	29	41.4	18	2	US-08-480-190-204	Sequence 204, App
6	29	41.4	18	2	US-08-488-379-204	Sequence 204, App
7	29	41.4	18	4	US-08-475-399A-204	Sequence 204, App
8	29	41.4	18	4	US-08-077-255A-204	Sequence 204, App
9	29	41.4	18	5	PCT-US93-07545-204	Sequence 204, App
10	28	40.0	5	1	US-08-477-509B-13	Sequence 13, Appl
11	28	40.0	5	3	US-08-482-085B-13	Sequence 13, Appl
12	28	40.0	5	3	US-09-444-791A-13	Sequence 13, Appl
13	28	40.0	15	1	US-08-230-047-31	Sequence 31, Appl
14	28	40.0	15	3	US-09-141-882A-10	Sequence 10, Appl
15	28	40.0	15	3	US-09-452-142-10	Sequence 10, Appl
16	28	40.0	17	4	US-09-355-398C-2	Sequence 2, Appli
17	28	40.0	18	4	US-09-355-398C-5	Sequence 5, Appli
18	28	40.0	19	3	US-08-943-173-8	Sequence 8, Appli
19	27	38.6	10	3	US-08-836-561-51	Sequence 51, Appl
20	27	38.6	10	4	US-09-434-122-51	Sequence 51, Appl
21	27	38.6	16	1	US-08-185-432-14	Sequence 14, Appl
22	27	38.6	16	4	US-09-715-923-8	Sequence 8, Appli
23	26.5	37.9	16	3	US-08-602-999A-204	Sequence 204, App
24	26.5	37.9	16	4	US-09-500-124-204	Sequence 204, App
25	26	37.1	9	1	US-08-615-181-100	Sequence 100, App
26	26	37.1	10	4	US-08-983-157B-8	Sequence 8, Appli
27	26	37.1	10	4	US-09-653-465B-11	Sequence 11, Appl
28	26	37.1	11	3	US-09-261-855-15	Sequence 15, Appl
29	26	37.1	11	4	US-09-873-637-15	Sequence 15, Appl
30	26	37.1	12	4	US-09-428-082B-519	Sequence 519, App
31	26	37.1	12	4	US-09-563-222C-43	Sequence 43, Appl
32	26	37.1	13	4	US-10-038-612-121	Sequence 121, App
33	26	37.1	14	1	US-08-191-866D-79	Sequence 79, Appl
34	26	37.1	14	2	US-08-185-949B-79	Sequence 79, Appl
35	26	37.1	14	2	US-08-634-001C-1	Sequence 1, Appli
36	26	37.1	14	3	US-09-470-618-15	Sequence 15, Appl
37	26	37.1	15	3	US-08-630-916A-100	Sequence 100, App
38	26	37.1	15	3	US-08-602-999A-322	Sequence 322, App
39	26	37.1	15	3	US-08-630-915A-156	Sequence 156, App
40	26	37.1	15	4	US-09-500-124-322	Sequence 322, App
41	26	37.1	15	4	US-09-879-957-156	Sequence 156, App
42	26	37.1	17	2	US-08-467-587A-33	Sequence 33, Appl
43	26	37.1	18	2	US-08-459-568-71	Sequence 71, Appl
44	26	37.1	18	2	US-08-399-411-71	Sequence 71, Appl
45	26	37.1	18	2	US-08-467-587A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-964-725-15
; Sequence 15, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: No. 5939265e
US-08-964-725-15

Query Match 50.0%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLSL 13
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Db 6 PVDKLAPLPL 15

RESULT 2
US-09-007-288E-88
; Sequence 88, Application US/09007288E
; Patent No. 6495357
; GENERAL INFORMATION:
; APPLICANT: Fuglsang, Claus
; APPLICANT: Okkels, Jens
; APPLICANT: Petersen, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Thellersen, Marianne
; APPLICANT: Svenden, Allan
; APPLICANT: Borch, Kim
; APPLICANT: Royer, John
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Halkier, Torben
; APPLICANT: Vind, Jesper
; APPLICANT: Jorgensen, Steen
; TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes
; FILE REFERENCE: 4455.404-US
; CURRENT APPLICATION NUMBER: US/09/007,288E
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide addition
US-09-007-288E-88

Query Match 47.1%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
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Db 3 PPRPRLLPIS 12

RESULT 3
US-09-400-653A-31
; Sequence 31, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/1F142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-400-653A-31

Query Match 42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
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Db 4 PPVSQELPCS 13

RESULT 4
US-09-248-061B-27
; Sequence 27, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S-T.
; APPLICANT: Lim, D-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/248,061B
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-27

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Best Local Similarity 60.0%; Pred. No. 70;
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Db 4 PPVSQELPCS 13

RESULT 5
US-08-480-190-204
; Sequence 204, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

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;      APPLICATION NUMBER:  08/077,255
;      FILING DATE:  June 15, 1993
;      APPLICATION NUMBER:  07/925,460
;      FILING DATE:  August 11, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00246/168001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-480-190-204

  Query Match             41.4%;  Score 29;  DB 2;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PVEKLLPLS 12
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Db          3 PYEKEVPLS 11


RESULT 6
US-08-488-379-204
; Sequence 204, Application US/08488379
; Patent No. 5880103
;  GENERAL INFORMATION:
;    APPLICANT:  Robert G. Urban
;    APPLICANT:  Roman M. Chicz
;    APPLICANT:  Dario A. A. Vignali
;    APPLICANT:  Mary L. Hedley
;    APPLICANT:  Lawrence J. Stern
;    APPLICANT:  Jack L. Strominger
;    TITLE OF INVENTION:  IMMUNOMODULATORY PEPTIDES
;    NUMBER OF SEQUENCES:  274
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,379
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/077,255
;      FILING DATE:  June 15, 1993
;      APPLICATION NUMBER:  07/925,460
;      FILING DATE:  August 11, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00246/168001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-488-379-204

  Query Match             41.4%;  Score 29;  DB 2;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PVEKLLPLS 12
              | || :|||
Db          3 PYEKEVPLS 11


RESULT 7
US-08-475-399A-204
; Sequence 204, Application US/08475399A
; Patent No. 6509033
;  GENERAL INFORMATION:
;    APPLICANT:  Urban, Robert G.
;    APPLICANT:  Chicz, Roman M.
;    APPLICANT:  Vignali, Dario A.A.
;    APPLICANT:  Hedley, Mary L.
;    APPLICANT:  Stern, Lawrence J.
;    APPLICANT:  Strominger, Jack L.
;    TITLE OF INVENTION:  IMMUNOMODULATORY PEPTIDES
;    NUMBER OF SEQUENCES:  276
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,399A
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/077,255
;      FILING DATE:  15-JUN-1993
;      APPLICATION NUMBER:  07/925,460
;      FILING DATE:  11-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00246/168003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-507
;      TELEFAX:  617/542-890
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-475-399A-204

  Query Match             41.4%;  Score 29;  DB 4;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PVEKLLPLS 12
              | || :|||
Db          3 PYEKEVPLS 11


RESULT 8
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US-08-077-255A-204
; Sequence 204, Application US/08077255A
; Patent No. 6696061
;  GENERAL INFORMATION:
;    APPLICANT:  Robert G. Urban
;    APPLICANT:  Roman M. Chicz
;    APPLICANT:  Dario A. A. Vignali
;    APPLICANT:  Mary L. Hedley
;    APPLICANT:  Lawrence J. Stern
;    APPLICANT:  Jack L. Strominger
;    TITLE OF INVENTION:  IMMUNOMODULATORY PEPTIDES
;    NUMBER OF SEQUENCES:  274
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/077,255A
;      FILING DATE:  June 15, 1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/925,460
;      FILING DATE:  August 11, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00246/168001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-077-255A-204

  Query Match             41.4%;  Score 29;  DB 4;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PVEKLLPLS 12
              | || :|||
Db          3 PYEKEVPLS 11


RESULT 9
PCT-US93-07545-204
; Sequence 204, Application PC/TUS9307545
;  GENERAL INFORMATION:
;    APPLICANT:  Robert G. Urban
;    APPLICANT:  Roman M. Chicz
;    APPLICANT:  Dario A. A. Vignali
;    APPLICANT:  Mary L. Hedley
;    APPLICANT:  Lawrence J. Stern
;    APPLICANT:  Jack L. Strominger
;    TITLE OF INVENTION:  IMMUNOMODULATORY PEPTIDES
;    NUMBER OF SEQUENCES:  273
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07545
;      FILING DATE:  19930811
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/925,460
;      FILING DATE:  August 11, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00246/168001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
PCT-US93-07545-204

  Query Match             41.4%;  Score 29;  DB 5;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PVEKLLPLS 12
              | || :|||
Db          3 PYEKEVPLS 11


RESULT 10
US-08-477-509B-13
; Sequence 13, Application US/08477509B
; Patent No. 5770697
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A
;    APPLICANT:  Cappello, Joseph
;    APPLICANT:  Crissman, John w
;    APPLICANT:  Dorman, Mary A
;    TITLE OF INVENTION:  No. 5770697el Peptides Comprising Repetitive
;    TITLE OF INVENTION:  Units of Amino Acids and DNA Sequences Encoding the Same
;    NUMBER OF SEQUENCES:  112
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,509B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,155
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,049
;      FILING DATE:  22-APR-1993
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/114,618
;      FILING DATE:  29-OCT-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/927,258
;      FILING DATE:  04-NOV-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-55186-7/RFT/MTK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-509B-13

  Query Match             40.0%;  Score 28;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEK 7
              |||||
Db          1 PPVEK 5


RESULT 11
US-08-482-085B-13
; Sequence 13, Application US/08482085B
; Patent No. 6018030
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A.
;    APPLICANT:  Richardson, Charles
;    APPLICANT:  Chambers, James
;    APPLICANT:  Causey, Stuart
;    APPLICANT:  Pollock, Thomas J.
;    APPLICANT:  Cappello, Joseph
;    APPLICANT:  Crissman, John W.
;    TITLE OF INVENTION:  No. 6018030el Peptides Comprising Repetitive
;    TITLE OF INVENTION:  Units of Amino Acids and DNA Sequences Encoding the Same
;    NUMBER OF SEQUENCES:  112
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,085B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/927,258
;      FILING DATE:  04-NOV-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/114,618
;      FILING DATE:  29-OCT-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,049
;      FILING DATE:  22-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,155
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-55186-6/RFT/MTK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-085B-13

  Query Match             40.0%;  Score 28;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEK 7
              |||||
Db          1 PPVEK 5


RESULT 12
US-09-444-791A-13
; Sequence 13, Application US/09444791A
; Patent No. 6355776
;   GENERAL INFORMATION:
;        APPLICANT: Ferrari, Franco A.
;                   Richardson, Charles
;                   Chambers, James
;                   Causey, Stuart
;                   Pollock, Thomas J.
;                   Cappello, Joseph
;                   Crissman, John W.
;        TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive
;                            Units of Amino Acids and DNA Sequences Encoding the Same
;        NUMBER OF SEQUENCES: 117
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/444,791A
;             FILING DATE: 22-No. 6355776-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/482,085
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/175,155
;             FILING DATE: 29-DEC-1993
;             APPLICATION NUMBER: US 08/053,049
;             FILING DATE: 22-APR-1993
;             APPLICATION NUMBER: US 07/114,618
;             FILING DATE: 29-OCT-1987
;             APPLICATION NUMBER: US 06/927,258
;             FILING DATE: 04-NOV-1986
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Trecartin, Richard F.
;             REGISTRATION NUMBER: 31,801
;             REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
;        TELECOMMUNICATION INFORMATION:
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;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;    INFORMATION FOR SEQ ID NO: 13:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 5 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-444-791A-13

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  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEK 7
              |||||
Db          1 PPVEK 5


RESULT 13
US-08-230-047-31
; Sequence 31, Application US/08230047
; Patent No. 5541109
;  GENERAL INFORMATION:
;    APPLICANT:  Searfoss III, George H.
;    APPLICANT:  Ivashchenko, Yuri D.
;    APPLICANT:  Jaye, Michael C.
;    TITLE OF INVENTION:  EXPRESSION CLONING OF C-SRC SH3 BINDING
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.0 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/230,047
;      FILING DATE:  19-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goodman, Rosanne
;      REGISTRATION NUMBER:  32,534
;      REFERENCE/DOCKET NUMBER:  A1465-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3817
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-230-047-31

  Query Match             40.0%;  Score 28;  DB 1;  Length 15;
  Best Local Similarity   44.4%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 PPVEKLLPL 11
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Db          6 PPLPQFLPM 14


RESULT 14
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US-09-141-882A-10
; Sequence 10, Application US/09141882A
; Patent No. 6022540
;  GENERAL INFORMATION:
;    APPLICANT:  Bruder, S. and Jaiswal, N.
;    TITLE OF INVENTION:  Ligands That Modulate
;    TITLE OF INVENTION:  Differentiation of Mesenchymal Stem Cells
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/141,882A
;      FILING DATE:  herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/057,928
;      FILING DATE:  September 4, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEMIONOW, R.
;      REGISTRATION NUMBER:  39,022
;      REFERENCE/DOCKET NUMBER:  640100-249
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  973-994-1700
;      TELEFAX:  973-994-1744
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  peptide
US-09-141-882A-10

  Query Match             40.0%;  Score 28;  DB 3;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NPPVEKLL 9
              ||| |: |
Db          6 NPPPEEFL 13


RESULT 15
US-09-452-142-10
; Sequence 10, Application US/09452142
; Patent No. 6379953
;  GENERAL INFORMATION:
;       APPLICANT: Bruder, S. and Jaiswal, N.
;       TITLE OF INVENTION: Ligands That Modulate
;                           Differentiation of Mesenchymal Stem Cells
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                       CECCHI, STEWART & OLSTEIN
;            STREET: 6 BECKER FARM ROAD
;            CITY: ROSELAND
;            STATE: NEW JERSEY
;            COUNTRY: USA
;            ZIP: 07068
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 INCH DISKETTE
;            COMPUTER: IBM PS/2
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;              FILING DATE: 01-Dec-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/141,882
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SEMIONOW, R.
;              REGISTRATION NUMBER: 39,022
;              REFERENCE/DOCKET NUMBER: 640100-249
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 973-994-1700
;              TELEFAX: 973-994-1744
;    INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 15 AMINO ACIDS
;              TYPE: AMINO ACID
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: LINEAR
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-452-142-10

  Query Match             40.0%;  Score 28;  DB 3;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NPPVEKLL 9
              ||| |: |
Db          6 NPPPEEFL 13


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Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

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Searched: 1370721 seqs, 324215800 residues

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Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	50.0	9	14	US-10-334-726-111	Sequence 111, App
2	33	47.1	12	14	US-10-232-544-88	Sequence 88, Appl
3	30	42.9	14	14	US-10-024-123-31	Sequence 31, Appl
4	29	41.4	15	14	US-10-072-602B-616	Sequence 616, App
5	29	41.4	17	15	US-10-378-089-1	Sequence 1, Appli
6	28	40.0	5	14	US-10-096-986-13	Sequence 13, Appl
7	28	40.0	8	15	US-10-182-252A-154	Sequence 154, App
8	28	40.0	9	15	US-10-264-309-397	Sequence 397, App
9	28	40.0	9	15	US-10-182-252A-142	Sequence 142, App
10	28	40.0	9	15	US-10-182-252A-273	Sequence 273, App
11	28	40.0	9	15	US-10-182-252A-796	Sequence 796, App
12	28	40.0	9	15	US-10-182-252A-840	Sequence 840, App
13	28	40.0	9	15	US-10-182-252A-1156	Sequence 1156, Ap
14	28	40.0	9	15	US-10-182-252A-1157	Sequence 1157, Ap
15	28	40.0	9	15	US-10-182-252A-1158	Sequence 1158, Ap
16	28	40.0	9	15	US-10-182-252A-1159	Sequence 1159, Ap
17	28	40.0	9	15	US-10-182-252A-1173	Sequence 1173, Ap
18	28	40.0	9	16	US-10-415-014-516	Sequence 516, App
19	28	40.0	9	16	US-10-415-014-624	Sequence 624, App
20	28	40.0	10	9	US-09-055-744-5	Sequence 5, Appli
21	28	40.0	10	16	US-10-415-014-572	Sequence 572, App
22	28	40.0	12	9	US-09-055-744-7	Sequence 7, Appli
23	28	40.0	14	14	US-10-148-936-2	Sequence 2, Appli
24	28	40.0	16	16	US-10-481-180-682	Sequence 682, App
25	28	40.0	18	9	US-09-880-713A-19	Sequence 19, Appl
26	28	40.0	18	9	US-09-226-248B-9	Sequence 9, Appli
27	27	38.6	8	15	US-10-182-252A-1296	Sequence 1296, Ap
28	27	38.6	9	15	US-10-182-252A-140	Sequence 140, App
29	27	38.6	9	15	US-10-182-252A-272	Sequence 272, App
30	27	38.6	9	15	US-10-182-252A-884	Sequence 884, App
31	27	38.6	9	15	US-10-182-252A-885	Sequence 885, App
32	27	38.6	9	15	US-10-182-252A-899	Sequence 899, App
33	27	38.6	9	15	US-10-182-252A-900	Sequence 900, App
34	27	38.6	10	14	US-10-283-349-51	Sequence 51, Appl
35	27	38.6	12	9	US-09-997-579-10	Sequence 10, Appl
36	27	38.6	12	14	US-10-360-522-6	Sequence 6, Appli
37	27	38.6	14	9	US-09-826-290-224	Sequence 224, App
38	27	38.6	14	14	US-10-162-134A-3	Sequence 3, Appli
39	27	38.6	14	15	US-10-264-309-47	Sequence 47, Appl
40	27	38.6	16	14	US-10-357-479-8	Sequence 8, Appli
41	27	38.6	17	14	US-10-225-567A-753	Sequence 753, App
42	27	38.6	18	14	US-10-225-567A-752	Sequence 752, App
43	27	38.6	19	9	US-09-997-579-8	Sequence 8, Appli
44	26.5	37.9	16	14	US-10-161-791-204	Sequence 204, App
45	26	37.1	8	9	US-09-055-744-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-334-726-111
; Sequence 111, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
; TITLE OF INVENTION: BREAST CANCER ANTIGEN
; FILE REFERENCE: 1090-36
; CURRENT APPLICATION NUMBER: US/10/334,726
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/645,446
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00866
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: GB 9805877.9
; PRIOR FILING DATE: 1998-09-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:predicted
; OTHER INFORMATION: peptide
US-10-334-726-111

Query Match 50.0%; Score 35; DB 14; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 PVEKLLPL 11
              |:||:|||
Db          1 PLEKILPL 8
```

```
RESULT 2
US-10-232-544-88
; Sequence 88, Application US/10232544
; Publication No. US20030199069A1
; GENERAL INFORMATION:
;  APPLICANT: Fuglsang, Claus
;  APPLICANT:  Okkels, Jens
;  APPLICANT:  Petersen, Dorte
;  APPLICANT:  Patkar, Shamkant
;  APPLICANT:  Thellersen, Marianne
;  APPLICANT:  Svenden, Allan
;  APPLICANT:  Borch, Kim
;  APPLICANT:  Royer, John
;  APPLICANT:  Kretzschmar, Titus
;  APPLICANT:  Halkier, Torben
;  APPLICANT:  Vind, Jesper
;  APPLICANT:  Jorgensen, Steen
;  TITLE OF INVENTION: No. US20030199069A1el Lipolytic Enzymes
;  FILE REFERENCE: 4455.404-US
;  CURRENT APPLICATION NUMBER: US/10/232,544
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: US/09/007,288
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide addition
US-10-232-544-88

  Query Match            47.1%;  Score 33;  DB 14;  Length 12;
  Best Local Similarity  60.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 PPVEKLLPLS 12
              ||  :|||:|
Db          3 PPRPRLLPIS 12


RESULT 3
US-10-024-123-31
; Sequence 31, Application US/10024123
; Publication No. US20030022263A1
; GENERAL INFORMATION:
;  APPLICANT: Kastan, Michael
;  APPLICANT:  Canman, Christine
;  APPLICANT:  Kim, Seong-Tae
;  APPLICANT:  Lim, Dae-Sik
;  APPLICANT:  St. Jude Children's Research Hospital
;  TITLE OF INVENTION: ATM Kinase Modulation for Screening and
;  TITLE OF INVENTION:  Therapies
;  FILE REFERENCE: 2427/1F142
;  CURRENT APPLICATION NUMBER: US/10/024,123
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/400,653
;  PRIOR FILING DATE: 1999-09-21
;  PRIOR APPLICATION NUMBER: 09/248,061
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-024-123-31

  Query Match            42.9%;  Score 30;  DB 14;  Length 14;
  Best Local Similarity  60.0%;  Pred. No. 4.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 PPVEKLLPLS 12
              ||| : || |
Db          4 PPVSQELPCS 13


RESULT 4
US-10-072-602B-616
; Sequence 616, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
;  APPLICANT: University of Utah Research Foundation
;  APPLICANT:  Cognetix, Inc.
;  APPLICANT:  Olivera, Baldomero M.
;  APPLICANT:  McIntosh, J, Michael
;  APPLICANT:  Watkins, Maren
;  APPLICANT:  Garrett, James E.
;  APPLICANT:  Cruz, Lourdes J.
;  APPLICANT:  Grilley, Michelle
;  APPLICANT:  Schoenfeld, Robert M.
;  APPLICANT:  Walker, Craig
;  APPLICANT:  Shetty, Reshma
;  APPLICANT:  Jones, Robert M.
;  TITLE OF INVENTION: Cone Snail Peptides
;  FILE REFERENCE: 2314-249
;  CURRENT APPLICATION NUMBER: US/10/072,602B
;  CURRENT FILING DATE:  2002-02-11
;  PRIOR APPLICATION NUMBER: US 60/267,408
;  PRIOR FILING DATE: 2001-02-09
;  NUMBER OF SEQ ID NOS: 638
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 616
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Conus flavidus
US-10-072-602B-616

  Query Match            41.4%;  Score 29;  DB 14;  Length 15;
  Best Local Similarity  60.0%;  Pred. No. 6.6e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 SNPPVEKLLP 10
              ||||   | |
Db          4 SNPPCSYLNP 13


RESULT 5
US-10-378-089-1
; Sequence 1, Application US/10378089
; Publication No. US20040052780A1
; GENERAL INFORMATION:
;  APPLICANT: ONO, KAZUHISA
;  APPLICANT:  KAWAMOTO, SEIJI
;  APPLICANT:  GOTO, TAKESHI
;  APPLICANT:  SATO, SHUJI
;  APPLICANT:  GOTO, SIGERU
;  TITLE OF INVENTION: IMMUNOSUPPRESANT
;  FILE REFERENCE: 7388/80237
;  CURRENT APPLICATION NUMBER: US/10/378,089
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: JP P2002-260681
;  PRIOR FILING DATE: 2002-09-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-378-089-1

  Query Match            41.4%;  Score 29;  DB 15;  Length 17;
  Best Local Similarity  55.6%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          1 SNPPVEKLL 9
              | ||| :|:
Db          5 SGPPVSELI 13


RESULT 6
US-10-096-986-13
; Sequence 13, Application US/10096986
; Publication No. US20030083464A1
;   GENERAL INFORMATION:
;        APPLICANT: Ferrari, Franco A.
;                   Richardson, Charles
;                   Chambers, James
;                   Causey, Stuart
;                   Pollock, Thomas J.
;                   Cappello, Joseph
;                   Crissman, John W.
;        TITLE OF INVENTION: No. US20030083464A1el Peptides Comprising Repetitive
;                            Units of Amino Acids and DNA Sequences Encoding the Same
;        NUMBER OF SEQUENCES: 117
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
;             STREET: Four Embarcadero Center, Suite 3400
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: US
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/096,986
;             FILING DATE: 12-Mar-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/444,791
;             FILING DATE: 22-No. US20030083464A1-1999
;             APPLICATION NUMBER: US 08/482,085
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/175,155
;             FILING DATE: 29-DEC-1993
;             APPLICATION NUMBER: US 08/053,049
;             FILING DATE: 22-APR-1993
;             APPLICATION NUMBER: US 07/114,618
;             FILING DATE: 29-OCT-1987
;             APPLICATION NUMBER: US 06/927,258
;             FILING DATE: 04-NOV-1986
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Trecartin, Richard F.
;             REGISTRATION NUMBER: 31,801
;             REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-781-1989
;             TELEFAX: 415-398-3249
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-096-986-13

  Query Match             40.0%;  Score 28;  DB 14;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEK 7
              |||||
Db          1 PPVEK 5


RESULT 7
US-10-182-252A-154
; Sequence 154, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-154

  Query Match             40.0%;  Score 28;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNPPV 5
              |||||
Db          2 SNPPV 6


RESULT 8
US-10-264-309-397
; Sequence 397, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
;  APPLICANT: DURHAM, L. KATHRYN
;  APPLICANT:  FRIEDMAN, DAVID L.
;  APPLICANT:  HERATH, HERATH
;  APPLICANT:  KIMMEL, LIDA H.
;  APPLICANT:  PAREKH, RAJESH B.
;  APPLICANT:  POTTER, DAVID M.
;  APPLICANT:  ROHLFF, CHRISTIAN
;  APPLICANT:  SILBER, B. MICHAEL
;  APPLICANT:  SNYDER, PETER J.
;  APPLICANT:  SOARES, HOLLY D.
;  APPLICANT:  STIGER, THOMAS R.
;  APPLICANT:  SUNDERLAND, P. TREY
;  APPLICANT:  TOWNSEND, ROBERT R.
;  APPLICANT:  WHITE, W. FROST
;  APPLICANT:  WILLIAMS, STEPHEN A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
;  TITLE OF INVENTION:  INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
;  FILE REFERENCE: POA-002.01
;  CURRENT APPLICATION NUMBER: US/10/264,309
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: 60/326,708
;  PRIOR FILING DATE: 2001-10-03
;  NUMBER OF SEQ ID NOS: 491
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 397
```

```
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-309-397

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 LPLSLK 14
              ||||||
Db          4 LPLSLK 9


RESULT 9
US-10-182-252A-142
; Sequence 142, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-142

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNPPV 5
              |||||
Db          3 SNPPV 7


RESULT 10
US-10-182-252A-273
; Sequence 273, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-273

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNPPV 5
              |||||
Db          3 SNPPV 7


RESULT 11
US-10-182-252A-796
; Sequence 796, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 796
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-796

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEKL 8
              ||:|:|
Db          4 PPIERL 9


RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
```

```
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 840
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-840

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPVEKL 8
              ||:|:|
Db          4 PPIERL 9


RESULT 13
US-10-182-252A-1156
; Sequence 1156, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1156
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1156

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNPPV 5
              |||||
Db          3 SNPPV 7


RESULT 14
US-10-182-252A-1157
; Sequence 1157, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1157
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1157

  Query Match             40.0%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNPPV 5
              |||||
Db          3 SNPPV 7


RESULT 15
US-10-182-252A-1158
; Sequence 1158, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
;  APPLICANT: FOMSGAARD, ANDERS
;  APPLICANT:  BRUNAK, SOREN
;  APPLICANT:  BUUS, SOREN
;  APPLICANT:  CORBET, SYLVIE
;  APPLICANT:  LAUEMOLLER, SANNE LISE
;  APPLICANT:  HANSEN, JAN
;  TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
;  TITLE OF INVENTION:  CONTROL OF HIV INFECTIONS
;  FILE REFERENCE: 030307/0205
;  CURRENT APPLICATION NUMBER: US/10/182,252A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: PCT/DK01/00059
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: EP 00610017.6
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 60/179,333
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 1388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1158
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1158
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Query Match 40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SNPPV 5
              |||||
Db          3 SNPPV 7
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Search completed: October 28, 2004, 19:45:44
Job time : 126 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 00:10:53 ; Search time 2574 Seconds
(without alignments)
257.209 Million cell updates/sec

Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1863394

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57
-USER=US09980881_@CGN_1_1_3731_@runat_28102004_131502_11397 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	46	65.7	43	6	AX093019	AX093019 Sequence
c 2	37	52.9	41	6	AX519039	AX519039 Sequence
3	36	51.4	51	6	CQ001968	CQ001968 Sequence
4	35.5	50.7	39	6	A24246	A24246 Oligonucleo
c 5	35	50.0	45	6	CQ767550	CQ767550 Sequence
c 6	35	50.0	45	6	AX201424	AX201424 Sequence
7	34	48.6	34	6	AR364159	AR364159 Sequence
8	34	48.6	40	6	AR053703	AR053703 Sequence
9	34	48.6	40	6	AR258638	AR258638 Sequence
c 10	34	48.6	40	6	AX107547	AX107547 Sequence
c 11	34	48.6	41	6	AR036483	AR036483 Sequence
c 12	34	48.6	41	6	AR069442	AR069442 Sequence
c 13	34	48.6	41	6	I73464	I73464 Sequence 16
14	34	48.6	48	6	BD243527	BD243527 Nucleotid
15	34	48.6	48	6	AX034950	AX034950 Sequence
16	34	48.6	51	6	AR077572	AR077572 Sequence
17	34	48.6	51	6	AR265635	AR265635 Sequence
18	33	47.1	36	6	AR088742	AR088742 Sequence
19	33	47.1	36	6	AR095469	AR095469 Sequence
20	33	47.1	36	6	AR112470	AR112470 Sequence
21	33	47.1	36	6	BD070735	BD070735 Vectors h
22	33	47.1	36	6	BD070761	BD070761 Vectors h
c 23	33	47.1	41	6	AR036485	AR036485 Sequence
c 24	33	47.1	41	6	AR069444	AR069444 Sequence
c 25	33	47.1	41	6	I73466	I73466 Sequence 18
26	33	47.1	44	6	BD091851	BD091851 Novel cyt
27	33	47.1	44	6	BD091885	BD091885 Packaging
28	33	47.1	46	6	A16157	A16157 primer. 10/
c 29	33	47.1	48	9	HS3B3VB19	X84265 H.sapiens m
c 30	33	47.1	48	9	HSU14066	U14066 Human cell
c 31	33	47.1	48	9	HSU14068	U14068 Human cell
32	33	47.1	50	6	CQ002840	CQ002840 Sequence
c 33	33	47.1	51	6	CQ003669	CQ003669 Sequence
c 34	33	47.1	51	6	AX165250	AX165250 Sequence
35	33	47.1	51	6	AX190175	AX190175 Sequence
36	32	45.7	20	6	AX379575	AX379575 Sequence
c 37	32	45.7	23	6	AX587292	AX587292 Sequence
38	32	45.7	32	6	BD061431	BD061431 Novel pol
39	32	45.7	33	6	AR268900	AR268900 Sequence
40	32	45.7	33	6	AR492234	AR492234 Sequence
c 41	32	45.7	39	10	S86280	S86280 TCR V beta
c 42	32	45.7	47	6	AR291010	AR291010 Sequence
43	32	45.7	51	6	CQ001695	CQ001695 Sequence
44	32	45.7	51	6	AX162153	AX162153 Sequence
45	32	45.7	51	6	AX162154	AX162154 Sequence

ALIGNMENTS

RESULT 1
AX093019/c
LOCUS AX093019 43 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 24 from Patent WO0118192.
ACCESSION AX093019
VERSION AX093019.1 GI:13509494
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 24 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES Location/Qualifiers
source 1. .43
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligo Desoxynucloetide containing StuI restriction site"
ORIGIN

Alignment Scores:
Pred. No.: 9.58 Length: 43
Score: 46.00 Matches: 9

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Percent Similarity:     90.91%          Conservative:  1
Best Local Similarity:  81.82%          Mismatches:    1
Query Match:            65.71%          Indels:        0
DB:                     6               Gaps:          0

US-09-980-881A-9 (1-14) x AX093019 (1-43)

Qy          1 SerAsnProProValGluLysLeuLeuProLeu 11
              ||||||||||||||:::   ||||||||||||
Db         38 TCGAACCCTCCCGTGAAAGGCCTTCTACCATTA 6

RESULT 2
AX519039/c
LOCUS       AX519039                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 5237 from Patent WO02052044.
ACCESSION   AX519039
VERSION     AX519039.1  GI:23569098
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 5237 04-JUL-2002;
            Riken (JP)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              381             Length:        41
Score:                  37.00           Matches:       7
Percent Similarity:     77.78%          Conservative:  0
Best Local Similarity:  77.78%          Mismatches:    2
Query Match:            52.86%          Indels:        0
DB:                     6               Gaps:          0

US-09-980-881A-9 (1-14) x AX519039 (1-41)

Qy          3 ProProValGluLysLeuLeuProLeu 11
              ||||||||||||      |||||||||
Db         33 CCACCTGTGGAGMCTTTCCTACCACTG 7

RESULT 3
CQ001968
LOCUS       CQ001968                  51 bp    DNA     linear   PAT 16-JAN-2004
DEFINITION  Sequence 608 from Patent WO0147944.
ACCESSION   CQ001968
VERSION     CQ001968.1  GI:41008600
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0147944-A 608 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Accession number cg43927434"
ORIGIN

Alignment Scores:
Pred. No.:              709             Length:        51
Score:                  36.00           Matches:       7
Percent Similarity:     76.92%          Conservative:  3
Best Local Similarity:  53.85%          Mismatches:    3
Query Match:            51.43%          Indels:        0
DB:                     6               Gaps:          0

US-09-980-881A-9 (1-14) x CQ001968 (1-51)

Qy          1 SerAsnProProValGluLysLeuLeuProLeuSerLeu 13
              |||   |||||||||   :::   ||||||::::::|||
Db          1 AGCAGGCCTCCTGTAGCTCGCTAATTACCCGTGACTTTA 39

RESULT 4
A24246
LOCUS       A24246                    39 bp    DNA     linear   PAT 04-DEC-1994
DEFINITION  Oligonucleotide.
ACCESSION   A24246
VERSION     A24246.1  GI:833653
KEYWORDS    .
SOURCE      Rattus rattus (black rat)
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   .
  TITLE     HUMANIZED INTERLEUKIN-2 RECEPTCRS ANTIBODIES
  JOURNAL   Patent: WO 9301289-A 30 21-JAN-1993;
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Rattus rattus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10117"
ORIGIN

Alignment Scores:
Pred. No.:              677             Length:        39
Score:                  35.50           Matches:       9
Percent Similarity:     83.33%          Conservative:  1
Best Local Similarity:  75.00%          Mismatches:    1
Query Match:            50.71%          Indels:        1
DB:                     6               Gaps:          1

US-09-980-881A-9 (1-14) x A24246 (1-39)

Qy          3 ProProValGluLysLeuLeuProLeuSerLeuLys 14
              |||||||||   ||||||||||||||:::   |||
Db          5 CCCCCGGTG---AAGCTGCTACCTCTTGCACAGAAA 37

RESULT 5
CQ767550/c
LOCUS       CQ767550                  45 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 17 from Patent EP1386931.
ACCESSION   CQ767550
VERSION     CQ767550.1  GI:45095665
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
  TITLE     Human neurotrimin homologue
  JOURNAL   Patent: EP 1386931-A 17 04-FEB-2004;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial Sequence"
ORIGIN
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Alignment Scores:
Pred. No.:              953           Length:        45
Score:                  35.00         Matches:       7
Percent Similarity:     80.00%        Conservative:  1
Best Local Similarity:  70.00%        Mismatches:    2
Query Match:            50.00%        Indels:        0
DB:                     6             Gaps:          0

US-09-980-881A-9 (1-14) x CQ767550 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 6
AX201424/c
LOCUS       AX201424                  45 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 103 from Patent WO0153486.
ACCESSION   AX201424
VERSION     AX201424.1  GI:15391230
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
            Stone,D.M., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of tumour
  JOURNAL   Patent: WO 0153486-A 103 26-JUL-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe."
ORIGIN

Alignment Scores:
Pred. No.:              953           Length:        45
Score:                  35.00         Matches:       7
Percent Similarity:     80.00%        Conservative:  1
Best Local Similarity:  70.00%        Mismatches:    2
Query Match:            50.00%        Indels:        0
DB:                     6             Gaps:          0

US-09-980-881A-9 (1-14) x AX201424 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 7
AR364159
LOCUS       AR364159                  34 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 42 from patent US 5256545.
ACCESSION   AR364159
VERSION     AR364159.1  GI:34426485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Brown,M.S., Goldstein,J.L., Russell,D.W. and Sudhof,T.C.
  TITLE     Sterol Regulatory Elements
  JOURNAL   Patent: US 5256545-A 42 26-OCT-1993;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.11e+03      Length:        34
Score:                  34.00         Matches:       7
Percent Similarity:     70.00%        Conservative:  0
Best Local Similarity:  70.00%        Mismatches:    3
Query Match:            48.57%        Indels:        0
DB:                     6             Gaps:          0

US-09-980-881A-9 (1-14) x AR364159 (1-34)

Qy          2 AsnProProValGluLysLeuLeuProLeu 11
              |||   |||       |||||||||||||||
Db          4 AATCACCCCACTGCAAAACTCCTCCCCCTG 33

RESULT 8
AR053703
LOCUS       AR053703                  40 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 127 from patent US 5834252.
ACCESSION   AR053703
VERSION     AR053703.1  GI:5978565
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Stemmer,W.Peter.Christiaan. and Lipshutz,R.J.
  TITLE     End-complementary polymerase reaction
  JOURNAL   Patent: US 5834252-A 127 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e+03      Length:        40
Score:                  34.00         Matches:       5
Percent Similarity:     90.00%        Conservative:  4
Best Local Similarity:  50.00%        Mismatches:    1
Query Match:            48.57%        Indels:        0
DB:                     6             Gaps:          0

US-09-980-881A-9 (1-14) x AR053703 (1-40)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              ||||||:::   :::|||:::|||||||:::
Db          3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 9
AR258638
LOCUS       AR258638                  40 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 127 from patent US 6489146.
ACCESSION   AR258638
VERSION     AR258638.1  GI:27309014
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Stemmer,W.P.C. and Lipshutz,R.J.
  TITLE     End-complementary polymerase reaction
  JOURNAL   Patent: US 6489146-A 127 03-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e+03      Length:        40
Score:                  34.00         Matches:       5
Percent Similarity:     90.00%        Conservative:  4
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Best Local Similarity:  50.00%        Mismatches:    1
Query Match:            48.57%        Indels:        0
DB:                     6             Gaps:          0

US-09-980-881A-9 (1-14) x AR258638 (1-40)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              |||||||:::   :::|||:::|||||||:::
Db          3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 10
AX107547/c
LOCUS       AX107547                  40 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 366 from Patent WO0123606.
ACCESSION   AX107547
VERSION     AX107547.1  GI:13923032
KEYWORDS    .
SOURCE      Bradyrhizobium japonicum
  ORGANISM  Bradyrhizobium japonicum
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE   1
  AUTHORS   Grabowski,R. and Berghof,K.
  TITLE     Nucleic acid molecules for detecting bacteria and phylogenetic
            units of bacteria
  JOURNAL   Patent: WO 0123606-A 366 05-APR-2001;
            Biotecon Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Bradyrhizobium japonicum"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:375"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e+03       Length:        40
Score:                  34.00          Matches:       5
Percent Similarity:     100.00%        Conservative:  4
Best Local Similarity:  55.56%         Mismatches:    0
Query Match:            48.57%         Indels:        0
DB:                     6              Gaps:          0

US-09-980-881A-9 (1-14) x AX107547 (1-40)

Qy          4 ProValGluLysLeuLeuProLeuSer 12
              |||:::|||:::|||:::|||:::|||
Db         40 CCAATCGAACGATTAGTACCGGTAAGC 14

RESULT 11
AR036483/c
LOCUS       AR036483                  41 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5872218.
ACCESSION   AR036483
VERSION     AR036483.1  GI:5953151
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
            Williams,L.Thomas.
  TITLE     Human platelet-derived growth factor receptor extracellular domain
            antibodies
  JOURNAL   Patent: US 5872218-A 16 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.32e+03       Length:        41
Score:                  34.00          Matches:       6
Percent Similarity:     100.00%        Conservative:  2
Best Local Similarity:  75.00%         Mismatches:    0
Query Match:            48.57%         Indels:        0
DB:                     6              Gaps:          0

US-09-980-881A-9 (1-14) x AR036483 (1-41)

Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14

RESULT 12
AR069442/c
LOCUS       AR069442                  41 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 16 from patent US 5891652.
ACCESSION   AR069442
VERSION     AR069442.1  GI:7220330
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Wolf,D., Tomlinson,J.E., Frettc,L.J., Giese,N.A., Escobedo,J.A. and
            Williams,L.Thomas.
  TITLE     Methods of using domains of extracellular region of human
            platelet-derived growth factor receptor polypeptides
  JOURNAL   Patent: US 5891652-A 16 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.32e+03       Length:        41
Score:                  34.00          Matches:       6
Percent Similarity:     100.00%        Conservative:  2
Best Local Similarity:  75.00%         Mismatches:    0
Query Match:            48.57%         Indels:        0
DB:                     6              Gaps:          0

US-09-980-881A-9 (1-14) x AR069442 (1-41)

Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14

RESULT 13
I73464/c
LOCUS       I73464                    41 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 16 from patent US 5686572.
ACCESSION   I73464
VERSION     I73464.1  GI:3009605
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Wolf,D., Tomlinson,J.E., Frettc,L.J., Giese,N.A., Escobedo,J.A. and
            Williams,L.Thomas.
  TITLE     Domains of extracellular region of human platelet derived growth
            factor receptor polypeptides
  JOURNAL   Patent: US 5686572-A 16 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.32e+03       Length:        41
Score:                  34.00          Matches:       6
Percent Similarity:     100.00%        Conservative:  2
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Best Local Similarity:  75.00%          Mismatches:     0
Query Match:            48.57%          Indels:         0
DB:                     6               Gaps:           0

US-09-980-881A-9 (1-14) x I73464 (1-41)

Qy          1 SerAsnProProValGluLysLeu 8
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Db         37 TCGAATCCGCCAGTTAAGGAACTT 14

RESULT 14
BD243527
LOCUS       BD243527                 48 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleotide fragment, probe, primer, reagent, and method for
            detecting nucleotide sequence derived from replication origin of
            pBR322.
ACCESSION   BD243527
VERSION     BD243527.1  GI:33053297
KEYWORDS    JP 2002537856-A/34.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Lamy,D.
  TITLE     Nucleotide fragment, probe, primer, reagent, and method for
            detecting nucleotide sequence derived from replication origin of
  JOURNAL   Patent: JP 2002537856-A 34 12-NOV-2002;
            TRANSGENE
COMMENT     OS   PBR322 plasmid
            PN   JP 2002537856-A/34
            PD   12-NOV-2002
            PF   03-MAR-2000 JP 2000603424
            PR   05-MAR-1999 FR     99/02968
            PI   DIDIER LAMY
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Nucleotide fragment, probe, primer, reagent, and method for
            CC           detecting
            CC   nucleotide sequence derived from replication origin of pBR322
            FH   Key             Location/Qualifiers
            FT   source          1. .48
            FT                   /organism='PBR322 plasmid'.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.53e+03        Length:         48
Score:                  34.00           Matches:        5
Percent Similarity:     90.00%          Conservative:   4
Best Local Similarity:  50.00%          Mismatches:     1
Query Match:            48.57%          Indels:         0
DB:                     6               Gaps:           0

US-09-980-881A-9 (1-14) x BD243527 (1-48)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
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Db         19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48

RESULT 15
AX034950
LOCUS       AX034950                 48 bp    DNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 34 from Patent WO0053803.
ACCESSION   AX034950
VERSION     AX034950.1  GI:11190875
KEYWORDS    .
SOURCE      Cloning vector pBR322
  ORGANISM  Cloning vector pBR322
            artificial sequences; vectors.
REFERENCE   1
  AUTHORS   Lamy,D.
  TITLE     Nucleotide fragment, probe, primer, reagent and method for
            detecting a nucleotide sequence derived from pbr322 replication
            origin
  JOURNAL   Patent: WO 0053803-A 34 14-SEP-2000;
            LAMY DIDIER (FR) ; TRANSGENE (FR)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Cloning vector pBR322"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:47470"
ORIGIN

Alignment Scores:
Pred. No.:              1.53e+03        Length:         48
Score:                  34.00           Matches:        5
Percent Similarity:     90.00%          Conservative:   4
Best Local Similarity:  50.00%          Mismatches:     1
Query Match:            48.57%          Indels:         0
DB:                     6               Gaps:           0

US-09-980-881A-9 (1-14) x AX034950 (1-48)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              ||||||:::   :::|||:::||||||:::
Db         19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48


Search completed: October 31, 2004, 03:01:07
Job time : 2580 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 01:58:08 ; Search time 85 Seconds
(without alignments)
117.071 Million cell updates/sec

Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 934402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57
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Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	48.6	34	6	5256545-42	Patent No. 5256545
2	34	48.6	40	2	US-08-425-684-127	Sequence 127, App
3	34	48.6	40	2	US-08-675-502-127	Sequence 127, App
4	34	48.6	40	4	US-09-245-802-127	Sequence 127, App
c 5	34	48.6	41	1	US-08-168-917-16	Sequence 16, Appl
c 6	34	48.6	41	2	US-08-460-510-16	Sequence 16, Appl
c 7	34	48.6	41	2	US-08-460-490-16	Sequence 16, Appl
c 8	34	48.6	41	5	PCT-US92-00730-16	Sequence 16, Appl
9	34	48.6	41	5	PCT-US92-10430-11	Sequence 11, Appl
10	34	48.6	51	2	US-08-350-260A-287	Sequence 287, App
11	34	48.6	51	4	US-09-104-337A-287	Sequence 287, App
12	33	47.1	36	2	US-08-816-155B-38	Sequence 38, Appl
13	33	47.1	36	3	US-08-815-809-23	Sequence 23, Appl
14	33	47.1	36	3	US-09-079-587-38	Sequence 38, Appl
c 15	33	47.1	41	1	US-08-168-917-18	Sequence 18, Appl
c 16	33	47.1	41	2	US-08-460-510-18	Sequence 18, Appl
c 17	33	47.1	41	2	US-08-460-490-18	Sequence 18, Appl
c 18	33	47.1	41	5	PCT-US92-00730-18	Sequence 18, Appl
19	33	47.1	41	5	PCT-US92-10430-13	Sequence 13, Appl
20	32	45.7	33	4	US-09-566-420-2	Sequence 2, Appli
21	32	45.7	33	4	US-10-201-764-2	Sequence 2, Appli
c 22	32	45.7	47	4	US-09-422-978-2745	Sequence 2745, Ap
23	32	45.7	54	1	US-08-373-124A-2192	Sequence 2192, Ap
24	32	45.7	54	1	US-08-435-628-2192	Sequence 2192, Ap
c 25	31	44.3	43	3	US-08-832-985-52	Sequence 52, Appl
c 26	31	44.3	43	4	US-09-410-903-33	Sequence 33, Appl
c 27	31	44.3	43	4	US-08-835-159-52	Sequence 52, Appl
c 28	31	44.3	47	1	US-08-093-884-31	Sequence 31, Appl
29	30	42.9	39	4	US-09-548-797B-151	Sequence 151, App
30	30	42.9	39	4	US-09-548-797B-152	Sequence 152, App
c 31	30	42.9	45	2	US-08-494-151-2	Sequence 2, Appli
c 32	30	42.9	47	4	US-09-422-978-522	Sequence 522, App
c 33	30	42.9	47	4	US-09-422-978-2073	Sequence 2073, Ap
c 34	30	42.9	50	2	US-08-709-368-2	Sequence 2, Appli
c 35	30	42.9	52	4	US-08-956-171E-2252	Sequence 2252, Ap
c 36	30	42.9	52	4	US-08-781-986A-2252	Sequence 2252, Ap
37	30	42.9	54	1	US-08-366-953A-23	Sequence 23, Appl
38	30	42.9	54	1	US-08-311-486C-1099	Sequence 1099, Ap
39	30	42.9	56	4	US-09-270-767-29728	Sequence 29728, A
c 40	29.5	42.1	44	3	US-08-865-960-9	Sequence 9, Appli
c 41	29.5	42.1	55	2	US-08-850-049-70	Sequence 70, Appl
c 42	29.5	42.1	55	2	US-08-850-049-71	Sequence 71, Appl
c 43	29.5	42.1	55	2	US-08-850-049-74	Sequence 74, Appl
c 44	29.5	42.1	55	2	US-08-050-478-70	Sequence 70, Appl
c 45	29.5	42.1	55	2	US-08-050-478-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
5256545-42
;Patent No. 5256545
; APPLICANT: BROWN, MICHAEL S.;GOLDSTEIN, JOSEPH L.;RUSSELL,
;DAVID W.;SUDHOF, THOMAS C.
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/425,852
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 33,330
; FILING DATE: 30-MAR-1987
; APPLICATION NUMBER: 33,081
; FILING DATE: 30-MAR-1987
;SEQ ID NO:42:
; LENGTH: 34
5256545-42

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Pred. No.:	61.2	Length:	34
Score:	34.00	Matches:	7
Percent Similarity:	70.00%	Conservative:	0
Best Local Similarity:	70.00%	Mismatches:	3
Query Match:	48.57%	Indels:	0
DB:	6	Gaps:	0

US-09-980-881A-9 (1-14) x 5256545-42 (1-34)

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Qy          2 AsnProProValGluLysLeuLeuProLeu 11
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Db          4 AATCACCCCACTGCAAAACTCCTCCCCCTG 33
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RESULT 2
US-08-425-684-127
; Sequence 127, Application US/08425684

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; Patent No. 5834252
;  GENERAL INFORMATION:
;    APPLICANT:  STEMMER PH.D., WILLEM P.C.
;    TITLE OF INVENTION:  END-COMPLEMENTARY POLYMERASE REACTION
;    NUMBER OF SEQUENCES:  136
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND AND TOWNSEND AND CREW
;      STREET:  ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,684
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DUNN ESQ., TRACY J.
;      REGISTRATION NUMBER:  34,587
;      REFERENCE/DOCKET NUMBER:  16528J-015400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
US-08-425-684-127

Alignment Scores:
Pred. No.:                75.3          Length:         40
Score:                    34.00         Matches:        5
Percent Similarity:       90.00%        Conservative:   4
Best Local Similarity:    50.00%        Mismatches:     1
Query Match:              48.57%        Indels:         0
DB:                       2             Gaps:           0

US-09-980-881A-9 (1-14) x US-08-425-684-127 (1-40)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              ||||||:::   :::|||:::|||||||:::
Db          3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 3
US-08-675-502-127
; Sequence 127, Application US/08675502
; Patent No. 5928905
;  GENERAL INFORMATION:
;    APPLICANT:  STEMMER PH.D., WILLEM P.C.
;    APPLICANT:  LIPSHUTZ, ROBERT J.
;    TITLE OF INVENTION:  END-COMPLEMENTARY POLYMERASE REACTION
;    NUMBER OF SEQUENCES:  136
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND AND TOWNSEND AND CREW
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,502
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,684
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/05480
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY, ESQ., MATTHEW B.
;      REGISTRATION NUMBER:  39,787
;      REFERENCE/DOCKET NUMBER:  16528J-015410US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
US-08-675-502-127

Alignment Scores:
Pred. No.:                75.3          Length:         40
Score:                    34.00         Matches:        5
Percent Similarity:       90.00%        Conservative:   4
Best Local Similarity:    50.00%        Mismatches:     1
Query Match:              48.57%        Indels:         0
DB:                       2             Gaps:           0

US-09-980-881A-9 (1-14) x US-08-675-502-127 (1-40)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              ||||||:::   :::|||:::|||||||:::
Db          3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 4
US-09-245-802-127
; Sequence 127, Application US/09245802
; Patent No. 6489146
;  GENERAL INFORMATION:
;    APPLICANT:  STEMMER PH.D., WILLEM P.C.
;    APPLICANT:  LIPSHUTZ, ROBERT J.
;    TITLE OF INVENTION:  END-COMPLEMENTARY POLYMERASE REACTION
;    NUMBER OF SEQUENCES:  136
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND AND TOWNSEND AND CREW
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/245,802
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/675,502
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/05480
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
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;      NAME:  MURPHY, ESQ., MATTHEW B.
;      REGISTRATION NUMBER:  39,787
;      REFERENCE/DOCKET NUMBER:  16528J-015410US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
US-09-245-802-127

Alignment Scores:
Pred. No.:              75.3          Length:         40
Score:                  34.00         Matches:        5
Percent Similarity:     90.00%        Conservative:   4
Best Local Similarity:  50.00%        Mismatches:     1
Query Match:            48.57%        Indels:         0
DB:                     4             Gaps:           0

US-09-980-881A-9 (1-14) x US-09-245-802-127 (1-40)

Qy          3 ProProValGluLysLeuLeuProLeuSer 12
              ||||||:::   :::|||:::||||||:::
Db          3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 5
US-08-168-917-16/c
; Sequence 16, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
US-08-168-917-16

Alignment Scores:
Pred. No.:              77.7          Length:         41
Score:                  34.00         Matches:        6
Percent Similarity:     100.00%       Conservative:   2
Best Local Similarity:  75.00%        Mismatches:     0
Query Match:            48.57%        Indels:         0
DB:                     1             Gaps:           0

US-09-980-881A-9 (1-14) x US-08-168-917-16 (1-41)

Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14

RESULT 6
US-08-460-510-16/c
; Sequence 16, Application US/08460510
; Patent No. 5872218
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,510
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
```

US-08-460-510-16

Alignment Scores:

Pred. No.:	77.7	Length:	41
Score:	34.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	75.00%	Mismatches:	0
Query Match:	48.57%	Indels:	0
DB:	2	Gaps:	0

US-09-980-881A-9 (1-14) x US-08-460-510-16 (1-41)

```
Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14
```

RESULT 7
US-08-460-490-16/c
; Sequence 16, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-460-490-16

Alignment Scores:

Pred. No.:	77.7	Length:	41
Score:	34.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	75.00%	Mismatches:	0
Query Match:	48.57%	Indels:	0
DB:	2	Gaps:	0

US-09-980-881A-9 (1-14) x US-08-460-490-16 (1-41)

```
Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14
```

RESULT 8
PCT-US92-00730-16/c
; Sequence 16, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00730
; FILING DATE: 19920128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
PCT-US92-00730-16

Alignment Scores:

Pred. No.:	77.7	Length:	41
Score:	34.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	75.00%	Mismatches:	0
Query Match:	48.57%	Indels:	0
DB:	5	Gaps:	0

US-09-980-881A-9 (1-14) x PCT-US92-00730-16 (1-41)

```
Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||:::::|||
Db         37 TCGAATCCGCCAGTTAAGGAACTT 14
```

```
RESULT 9
PCT-US92-10430-11
; Sequence 11, Application PC/TUS9210430
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    TITLE OF INVENTION:  Methods for Production of Purified
;    TITLE OF INVENTION:  Soluble Type B and Type A Human Platelet-Derived Growth
;    TITLE OF INVENTION:  Factor Receptor Fragments
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10430
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/801,794
;      FILING DATE:  02-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  12418-15
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US92-10430-11

Alignment Scores:
Pred. No.:                77.7          Length:        41
Score:                    34.00         Matches:       6
Percent Similarity:       100.00%       Conservative:  2
Best Local Similarity:    75.00%        Mismatches:    0
Query Match:              48.57%        Indels:        0
DB:                       5             Gaps:          0

US-09-980-881A-9 (1-14) x PCT-US92-10430-11 (1-41)

Qy          1 SerAsnProProValGluLysLeu 8
              ||||||||||||||||:::::|||
Db          5 TCGAATCCGCCAGTTAAGGAACTT 28

RESULT 10
US-08-350-260A-287
; Sequence 287, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;    APPLICANT:  Winter, Gregory Paul
;    APPLICANT:  Griffiths, Andrew David
;    APPLICANT:  Williams, Samuel Cameron
;    APPLICANT:  Waterhouse, Peter
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Johnson, Kevin Stuart
;    APPLICANT:  Smith, Andrew John Hammond
;    TITLE OF INVENTION:  Methods for producing members of specific
;    TITLE OF INVENTION:  binding pairs
;    NUMBER OF SEQUENCES:  602
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough
;      STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,260A
;      FILING DATE:  05-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9110549.4
;      FILING DATE:  15-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01134
;      FILING DATE:  10-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00605
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  287:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  51 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-350-260A-287

Alignment Scores:
Pred. No.:                103           Length:        51
Score:                    34.00         Matches:       7
Percent Similarity:       77.78%        Conservative:  0
Best Local Similarity:    77.78%        Mismatches:    2
Query Match:              48.57%        Indels:        0
DB:                       2             Gaps:          0

US-09-980-881A-9 (1-14) x US-08-350-260A-287 (1-51)

Qy          3 ProProValGluLysLeuLeuProLeu 11
              ||||||      ||||||||||||||
Db         11 CCGCCGAATACGAAGTTGCTCCCACTG 37

RESULT 11
US-09-104-337A-287
; Sequence 287, Application US/09104337A
; Patent No. 6492160
;  GENERAL INFORMATION:
;       APPLICANT: Winter, Gregory Paul
```

```
;                  Griffiths, Andrew David
;                  Williams, Samuel Cameron
;                  Waterhouse, Peter
;                  Nissim, Ahuva
;                  Johnson, Kevin Stuart
;                  Smith, Andrew John Hammond
;       TITLE OF INVENTION: Methods for producing members of specific
;                           binding pairs
;       NUMBER OF SEQUENCES: 600
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Audrey L. Bartnicki
;            STREET: Marshall, Gerstein & Borun
;                    6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/104,337A
;            FILING DATE: 25-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/350,260
;            FILING DATE: 05-DEC-1994
;            APPLICATION NUMBER: GB 9110549.4
;            FILING DATE: 15-MAY-1991
;            APPLICATION NUMBER: GB 9206318.9
;            FILING DATE: 24-MAR-1992
;            APPLICATION NUMBER: PCT/GB92/00883
;            FILING DATE: 15-MAY-1992
;            APPLICATION NUMBER: PCT/GB93/00605
;            FILING DATE: 24-MAR-1993
;            APPLICATION NUMBER: US 08/150,002
;            FILING DATE: 31-MAR-1994
;            APPLICATION NUMBER: US 08/307,619
;            FILING DATE: 16-SEP-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bartnicki, Audrey L.
;            REGISTRATION NUMBER: 40,499
;            REFERENCE/DOCKET NUMBER: 28111/32372A
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312-474-6300
;  INFORMATION FOR SEQ ID NO: 287:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 51 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-09-104-337A-287

Alignment Scores:
Pred. No.:              103           Length:        51
Score:                  34.00         Matches:       7
Percent Similarity:     77.78%        Conservative:  0
Best Local Similarity:  77.78%        Mismatches:    2
Query Match:            48.57%        Indels:        0
DB:                     4             Gaps:          0

US-09-980-881A-9 (1-14) x US-09-104-337A-287 (1-51)

Qy          3 ProProValGluLysLeuLeuProLeu 11
              ||||||      ||||||||||||||||
Db         11 CCGCCGAATACGAAGTTGCTCCCACTG 37

RESULT 12
US-08-816-155B-38
; Sequence 38, Application US/08816155B
; Patent No. 5990091
;  GENERAL INFORMATION:
;    APPLICANT:  TARTAGLIA, JAMES
;    APPLICANT:  COX, WILLIAM I.
;    APPLICANT:  GETTIG, RUSSELL R.
;    APPLICANT:  MARTINEZ, HECTOR
;    APPLICANT:  PAOLETTI, ENZO
;    APPLICANT:  PINCUS, STEVEN E.
;    TITLE OF INVENTION:  VECTORS HAVING ENHANCED EXPRESSION, AND
;    TITLE OF INVENTION:  METHODS OF MAKING AND USES THEREOF
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FROMMER LAWRENCE & HAUG LLP
;      STREET:  745 FIFTH AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10151
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/816,155B
;      FILING DATE:  12-MAR-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOWALSKI, THOMAS J.
;      REGISTRATION NUMBER:  32,147
;      REFERENCE/DOCKET NUMBER:  454310-2990
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-588-0800
;      TELEFAX:  212-588-0500
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-816-155B-38

Alignment Scores:
Pred. No.:              101           Length:        36
Score:                  33.00         Matches:       6
Percent Similarity:     75.00%        Conservative:  0
Best Local Similarity:  75.00%        Mismatches:    2
Query Match:            47.14%        Indels:        0
DB:                     2             Gaps:          0

US-09-980-881A-9 (1-14) x US-08-816-155B-38 (1-36)

Qy          3 ProProValGluLysLeuLeuPro 10
              ||||||   |||||||||   |||
Db          1 CCCCCTGCAGAAAAATTAAGGCCC 24

RESULT 13
US-08-815-809-23
; Sequence 23, Application US/08815809
; Patent No. 6004777
; GENERAL INFORMATION:
;  APPLICANT: TARTAGLIA, James
;  APPLICANT: GOEBEL, Scott J.
;  APPLICANT: COX, William I.
;  APPLICANT: GETTIG, Russell R.
;  APPLICANT: PINCUS, Steven E.
;  APPLICANT: PAOLETTI, Enzo
;  APPLICANT: JACOBS, Bertram L.
;  TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
;  TITLE OF INVENTION: MAKING AND USES THEREOF
;  FILE REFERENCE: 454310-3010
;  CURRENT APPLICATION NUMBER: US/08/815,809
;  CURRENT FILING DATE: 1997-03-12
```

```
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Vaccinia virus
US-08-815-809-23

Alignment Scores:
Pred. No.:              101          Length:         36
Score:                  33.00        Matches:        6
Percent Similarity:     75.00%       Conservative:   0
Best Local Similarity:  75.00%       Mismatches:     2
Query Match:            47.14%       Indels:         0
DB:                     3            Gaps:           0

US-09-980-881A-9 (1-14) x US-08-815-809-23 (1-36)

Qy          3 ProProValGluLysLeuLeuPro 10
              ||||||   |||||||||   |||
Db          1 CCCCCTGCAGAAAAATTAAGGCCC 24

RESULT 14
US-09-079-587-38
; Sequence 38, Application US/09079587
; Patent No. 6130066
;  GENERAL INFORMATION:
;    APPLICANT:  TARTAGLIA, JAMES
;    APPLICANT:  COX, WILLIAM I.
;    APPLICANT:  GETTIG, RUSSELL R.
;    APPLICANT:  MARTINEZ, HECTOR
;    APPLICANT:  PAOLETTI, ENZO
;    APPLICANT:  PINCUS, STEVEN E.
;    TITLE OF INVENTION:  VECTORS HAVING ENHANCED EXPRESSION, AND
;    TITLE OF INVENTION:  METHODS OF MAKING AND USES THEREOF
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FROMMER LAWRENCE & HAUG LLP
;      STREET:  745 FIFTH AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10151
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,587
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/816,155
;      FILING DATE:  12-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOWALSKI, THOMAS J.
;      REGISTRATION NUMBER:  32,147
;      REFERENCE/DOCKET NUMBER:  454310-2990
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-588-0800
;      TELEFAX:  212-588-0500
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-079-587-38

Alignment Scores:
Pred. No.:              101          Length:         36
Score:                  33.00        Matches:        6
Percent Similarity:     75.00%       Conservative:   0
Best Local Similarity:  75.00%       Mismatches:     2
Query Match:            47.14%       Indels:         0
DB:                     3            Gaps:           0

US-09-980-881A-9 (1-14) x US-09-079-587-38 (1-36)

Qy          3 ProProValGluLysLeuLeuPro 10
              ||||||   |||||||||   |||
Db          1 CCCCCTGCAGAAAAATTAAGGCCC 24

RESULT 15
US-08-168-917-18/c
; Sequence 18, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
US-08-168-917-18

Alignment Scores:
Pred. No.:              119          Length:         41
Score:                  33.00        Matches:        7
Percent Similarity:     77.78%       Conservative:   0
Best Local Similarity:  77.78%       Mismatches:     2
Query Match:            47.14%       Indels:         0
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DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-18 (1-41)

```
Qy          1 SerAsnProProValGluLysLeuLeu 9
              ||||||||||||||||      ||||||
Db         37 TCGAATCCGCCAGTTATGATGTTGCTT 11
```

Search completed: October 31, 2004, 03:42:04
Job time : 88 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 03:01:14 ; Search time 366 Seconds
(without alignments)
196.138 Million cell updates/sec

Title: US-09-980-881A-9
Perfect score: 70
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 1975758

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	37	52.9	41	16	US-10-035-833A-5237	Sequence 5237, Ap
c	3	35	50.0	45	9	US-09-978-295A-17	Sequence 17, Appl
c	4	35	50.0	45	9	US-09-978-697-17	Sequence 17, Appl
c	5	35	50.0	45	9	US-09-978-192A-17	Sequence 17, Appl
c	6	35	50.0	45	9	US-09-999-832A-17	Sequence 17, Appl
c	7	35	50.0	45	10	US-09-978-189-17	Sequence 17, Appl
c	8	35	50.0	45	10	US-09-978-608A-17	Sequence 17, Appl
c	9	35	50.0	45	10	US-09-978-585A-17	Sequence 17, Appl
c	10	35	50.0	45	10	US-09-978-191A-17	Sequence 17, Appl
c	11	35	50.0	45	10	US-09-978-403A-17	Sequence 17, Appl
c	12	35	50.0	45	10	US-09-978-564A-17	Sequence 17, Appl
c	13	35	50.0	45	10	US-09-999-833A-17	Sequence 17, Appl
c	14	35	50.0	45	10	US-09-981-915A-17	Sequence 17, Appl
c	15	35	50.0	45	10	US-09-978-824-17	Sequence 17, Appl
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c	23	35	50.0	45	10	US-09-978-643A-17	Sequence 17, Appl
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c	25	35	50.0	45	10	US-09-978-298A-17	Sequence 17, Appl
c	26	35	50.0	45	10	US-09-978-188A-17	Sequence 17, Appl
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c	40	35	50.0	45	15	US-10-166-709A-17	Sequence 17, Appl
c	41	35	50.0	45	15	US-10-143-031A-17	Sequence 17, Appl
c	42	35	50.0	45	15	US-10-143-030A-17	Sequence 17, Appl
c	43	35	50.0	45	15	US-10-002-967A-17	Sequence 17, Appl
c	44	35	50.0	45	15	US-10-017-083A-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 24, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Oligo
; OTHER INFORMATION: Desoxynucloetide containing StuI restriction site

US-09-845-064-24

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US-09-980-881A-9 (1-14) x US-09-845-064-24 (1-43)

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; Sequence 5237, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5237
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-5237

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RESULT 3
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; Sequence 17, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

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US-09-980-881A-9 (1-14) x US-09-978-295A-17 (1-45)

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; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	9	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-978-697-17 (1-45)

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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 5
US-09-978-192A-17/c
; Sequence 17, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Alignment Scores:

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US-09-980-881A-9 (1-14) x US-09-978-192A-17 (1-45)

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Shelton, David L.

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; TITLE OF INVENTION: Acids Encoding the Same
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Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	9	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-999-832A-17 (1-45)

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RESULT 7
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; Sequence 17, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-978-189-17 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 8
US-09-978-608A-17/c
; Sequence 17, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-608A-17

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-978-608A-17 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 9
US-09-978-585A-17/c
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; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
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; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-585A-17

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
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US-09-980-881A-9 (1-14) x US-09-978-585A-17 (1-45)

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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 10
US-09-978-191A-17/c
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; Publication No. US20030050239A1
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores:
Pred. No.:                382             Length:         45
Score:                    35.00           Matches:        7
Percent Similarity:       80.00%          Conservative:   1
Best Local Similarity:    70.00%          Mismatches:     2
Query Match:              50.00%          Indels:         0
DB:                       10              Gaps:           0

US-09-980-881A-9 (1-14) x US-09-978-191A-17 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 11
US-09-978-403A-17/c
; Sequence 17, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-403A-17 (1-45)

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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 12
US-09-978-564A-17/c
; Sequence 17, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7

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Percent Similarity:     80.00%          Conservative:  1
Best Local Similarity:  70.00%          Mismatches:    2
Query Match:            50.00%          Indels:        0
DB:                     10              Gaps:          0

US-09-980-881A-9 (1-14) x US-09-978-564A-17 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
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RESULT 13
US-09-999-833A-17/c
; Sequence 17, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C65
;  CURRENT APPLICATION NUMBER: US/09/999,833A
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-999-833A-17 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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RESULT 14
US-09-981-915A-17/c
; Sequence 17, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

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US-09-980-881A-9 (1-14) x US-09-981-915A-17 (1-45)

Qy          1 SerAsnProProValGluLysLeuLeuPro 10
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Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 15
US-09-978-824-17/c
; Sequence 17, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C14
;  CURRENT APPLICATION NUMBER: US/09/978,824
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;  PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-978-824-17 (1-45)

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Qy          1 SerAsnProProValGluLysLeuLeuPro 10
              ||||||   ||||||:::   |||||||||
Db         32 AGCAATGCCCCGGTTCAAGGCCTGCTCCCC 3
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Search completed: October 31, 2004, 04:34:55
Job time : 370 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 28, 2004, 18:47:56 ; Search time 44.5 Seconds
(without alignments)
4688.459 Million cell updates/sec

Title: US-09-980-881A-1
Perfect score: 2777
Sequence: 1 agaaaattgctgttgggatg.....aaaaaaaaaaaaaaaaaaa 1573

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09980881/runat_28102004_131901_29505/app_query.fasta_1.1735
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09980881_@CGN_1_1_46_@runat_28102004_131901_29505 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1902.5	68.5	386	4	US-09-813-133A-2	Sequence 2, Appli
2	1885	67.9	423	1	US-07-649-591B-3	Sequence 3, Appli
3	1885	67.9	423	1	US-08-277-540-3	Sequence 3, Appli
4	1885	67.9	423	1	US-08-430-787A-3	Sequence 3, Appli
5	1885	67.9	423	2	US-08-869-057-2	Sequence 2, Appli
6	1874	67.5	423	4	US-09-813-133A-4	Sequence 4, Appli
7	655	23.6	417	1	US-07-649-591B-7	Sequence 7, Appli
8	655	23.6	417	1	US-08-277-540-7	Sequence 7, Appli
9	655	23.6	417	1	US-08-430-787A-7	Sequence 7, Appli
10	651.5	23.5	415	2	US-08-860-882A-57	Sequence 57, Appl
11	651.5	23.5	415	4	US-09-011-769A-39	Sequence 39, Appl
12	647.5	23.3	417	1	US-07-649-591B-6	Sequence 6, Appli
13	647.5	23.3	417	1	US-08-277-540-6	Sequence 6, Appli
14	647.5	23.3	417	1	US-08-430-787A-6	Sequence 6, Appli
15	647.5	23.3	417	4	US-09-917-254-66	Sequence 66, Appl
16	644	23.2	424	4	US-09-011-769A-56	Sequence 56, Appl
17	640.5	23.1	404	1	US-08-696-139-2	Sequence 2, Appli
18	635.5	22.9	437	4	US-09-675-305-10	Sequence 10, Appl
19	635.5	22.9	437	4	US-10-200-344-10	Sequence 10, Appl
20	634.5	22.8	716	3	US-09-171-945-125	Sequence 125, App
21	607.5	21.9	307	2	US-08-782-760-6	Sequence 6, Appli
22	607.5	21.9	307	5	PCT-US96-00995-6	Sequence 6, Appli
23	607	21.9	396	1	US-07-649-591B-4	Sequence 4, Appli
24	607	21.9	396	1	US-08-277-540-4	Sequence 4, Appli
25	607	21.9	396	1	US-08-430-787A-4	Sequence 4, Appli
26	576	20.7	306	1	US-08-696-139-4	Sequence 4, Appli
27	575	20.7	349	4	US-09-011-769A-47	Sequence 47, Appl
28	572.5	20.6	329	4	US-09-011-769A-51	Sequence 51, Appl
29	571.5	20.6	613	3	US-09-171-945-113	Sequence 113, App
30	568	20.5	349	4	US-09-011-769A-60	Sequence 60, Appl
31	567	20.4	349	4	US-09-011-769A-64	Sequence 64, Appl
32	553	19.9	417	1	US-07-649-591B-8	Sequence 8, Appli
33	553	19.9	417	1	US-08-277-540-8	Sequence 8, Appli
34	553	19.9	417	1	US-08-430-787A-8	Sequence 8, Appli
35	546.5	19.7	399	4	US-09-710-099-8	Sequence 8, Appli
36	546.5	19.7	399	4	US-10-200-910-8	Sequence 8, Appli
37	529.5	19.1	350	4	US-09-675-305-12	Sequence 12, Appl
38	529.5	19.1	350	4	US-10-200-344-12	Sequence 12, Appl
39	529	19.0	419	1	US-07-649-591B-5	Sequence 5, Appli
40	529	19.0	419	1	US-08-277-540-5	Sequence 5, Appli
41	529	19.0	419	1	US-08-430-787A-5	Sequence 5, Appli
42	520	18.7	436	4	US-09-710-099-6	Sequence 6, Appli
43	520	18.7	436	4	US-10-200-910-6	Sequence 6, Appli
44	513	18.5	417	3	US-08-640-906-4	Sequence 4, Appli
45	513	18.5	417	3	US-09-395-936-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Alignment Scores:
Pred. No.: 3.68e-202 Length: 386
Score: 1902.50 Matches: 363
Percent Similarity: 94.30% Conservative: 1
Best Local Similarity: 94.04% Mismatches: 5
Query Match: 68.51% Indels: 18
DB: 4 Gaps: 1

US-09-980-881A-1 (1-1573) x US-09-813-133A-2 (1-386)

Qy 18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
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Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy 78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
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Db        21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy       138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy       198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy       258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy       318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy       378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy       438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy       498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
             |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy       558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 617
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200

Qy       618 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGC 677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220

Qy       678 AACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 737
             ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       221 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240

Qy       738 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260

Qy       798 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280

Qy       858 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300

Qy       918 AGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCAT 977
             ||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db       301 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 320

Qy       978 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340

Qy      1038 ATCAAATATTCGTT---------------------------------------------- 1051
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Db       341 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 360

Qy      1052 ------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGG 1105
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrp 380

Qy      1106 CATGTCATTAGGAATGTT 1123
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Db       381 HisValIleArgAsnVal 386
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RESULT 2
US-07-649-591B-3
; Sequence 3, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-3

Alignment Scores:
Pred. No.:                3.37e-200       Length:          423
Score:                    1885.00         Matches:         365
Percent Similarity:       86.52%          Conservative:    1
Best Local Similarity:    86.29%          Mismatches:      3
Query Match:              67.88%          Indels:          55
DB:                       1               Gaps:            2

US-09-980-881A-1 (1-1573) x US-07-649-591B-3 (1-423)

Qy          18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy          78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy         138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy         198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy         258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
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Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy        608 ------------------------------------------------------------ 608

Db        201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db        221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT-------------------------------------------------------TAC 1054
              |||                                                       |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
              |||||||||
Db        421 ArgAsnVal 423

RESULT 3
US-08-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-3

Alignment Scores:
Pred. No.:              3.37e-200       Length:         423
Score:                  1885.00         Matches:        365
Percent Similarity:     86.52%          Conservative:   1
Best Local Similarity:  86.29%          Mismatches:     3
Query Match:            67.88%          Indels:         55
DB:                     1               Gaps:           2

US-09-980-881A-1 (1-1573) x US-08-277-540-3 (1-423)

Qy          18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy          78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy         138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy         198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy         258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
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Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
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Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy        608 ------------------------------------------------------------ 608

Db        201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy        609 -------------------------------------------AATCGAATGTGGAGAAAG 626
                                                        ||||||||||||||||||
Db        221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT----------------------------------------------------TAC 1054
              |||                                                    |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
              |||||||||
Db        421 ArgAsnVal 423

RESULT 4
US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-3

Alignment Scores:
Pred. No.:              3.37e-200       Length:         423
Score:                  1885.00         Matches:        365
Percent Similarity:     86.52%          Conservative:   1
Best Local Similarity:  86.29%          Mismatches:     3
Query Match:            67.88%          Indels:         55
DB:                     1               Gaps:           2

US-09-980-881A-1 (1-1573) x US-08-430-787A-3 (1-423)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy       318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy       378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy       438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy       498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy       558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy       608 ------------------------------------------------------------ 608

Db       201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy       609 ------------------------------------------AATCGAATGTGGAGAAAG 626
                                                       ||||||||||||||||||
Db       221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy       627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy       687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy       747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy       807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProProTyr 320

Qy       867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy       927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
             ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy       987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy      1047 TCGTT-------------------------------------------------------TAC 1054
             |||                                                         |||
Db       381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy      1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy      1115 AGGAATGTT 1123
             |||||||||
Db       421 ArgAsnVal 423

RESULT 5
US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Plasma
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23..401
US-08-869-057-2

Alignment Scores:
Pred. No.:              3.37e-200       Length:         423
Score:                  1885.00         Matches:        365
Percent Similarity:     86.52%          Conservative:   1
Best Local Similarity:  86.29%          Mismatches:     3
Query Match:            67.88%          Indels:         55
DB:                     2               Gaps:           2

US-09-980-881A-1 (1-1573) x US-08-869-057-2 (1-423)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
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Qy       318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
Db       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy       378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
Db       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy       438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
Db       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy       498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
Db       161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy       558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
Db       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy       608 ------------------------------------------------------------ 608
Db       201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy       609 ----------------------------------------AATCGAATGTGGAGAAAG 626
Db       221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy       627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
Db       241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy       687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
Db       261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280

Qy       747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
Db       281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy       807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
Db       301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyr 320

Qy       867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
Db       321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy       927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
Db       341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy       987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
Db       361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy      1047 TCGTT-----------------------------------------------------TAC 1054
Db       381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy      1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
Db       401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy      1115 AGGAATGTT 1123
Db       421 ArgAsnVal 423
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RESULT 6
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294

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; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4
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Alignment Scores:

Pred. No.:	5.6e-199	Length:	423
Score:	1874.00	Matches:	363
Percent Similarity:	86.05%	Conservative:	1
Best Local Similarity:	85.82%	Mismatches:	5
Query Match:	67.48%	Indels:	55
DB:	4	Gaps:	2

US-09-980-881A-1 (1-1573) x US-09-813-133A-4 (1-423)

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Qy        18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
Db         1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy        78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
Db        21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy       138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
Db        41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy       198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
Db        61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy       258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
Db        81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy       318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
Db       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy       378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
Db       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy       438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
Db       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy       498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
Db       161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy       558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
Db       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy       608 ------------------------------------------------------------ 608
Db       201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy       609 ----------------------------------------AATCGAATGTGGAGAAAG 626
Db       221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
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Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              ||||||||||||:::|||  ||||||||||||||||||||||||||||||||||||||||
Db        341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT----------------------------------------------------TAC 1054
              |||                                                    |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
              |||||||||
Db        421 ArgAsnVal 423

RESULT 7
US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-7

Alignment Scores:
Pred. No.:                1.14e-63        Length:          417
Score:                    655.00          Matches:         150
Percent Similarity:       51.67%          Conservative:    66
Best Local Similarity:    35.89%          Mismatches:      138
Query Match:              23.59%          Indels:          65
DB:                       1               Gaps:            9

US-09-980-881A-1 (1-1573) x US-07-649-591B-7 (1-417)

Qy         33 CTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCGTTCCAGAGT 92
              :::||||||:::         :::              |||         |||
Db          7 MetAlaValIleTyrThrThrLeuAlaIleAlaProValHis---------PheAspArg 23

Qy         93 GGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAATCTT 152
                 :::|||              :::     :::          ||||||:::||||||
Db         24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43

Qy        153 ACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAA 212
              |||   :::   |||:::     |||   |||                  |||
Db         44 ThrGlnSerIleGluLeuAspPheTrpTyrProAspAlaIleHisAspIleAlaValAsn 63

Qy        213 AAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTAAAT 272
                 |||   |||   |||:::     :::         :::::::::   |||
Db         64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83

Qy        273 GTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATTCAACAGCAG 332
                    |||         :::|||:::   |||:::::::::   |||::::::|||
Db         84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluGluIleGluLysGln 103

Qy        333 ATTTCC---AACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAGTATCAC 389
                  |||   ::::::  |||  |||        |||   :::|||:::
Db        104 PheAspValLysAspGluIleAlaGlyArgHisSer---------TyrAlaLysTyrAsn 120

Qy        390 TCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTT 449
                 ::::::|||   ||||||   |||   :::   |||:::||||||:::|||:::
Db        121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140

Qy        450 ACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAGGTTTCT 509
              ::::::|||   ||||||||:::   |||      ||||||||||||||||:::
Db        141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159

Qy        510 GGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAA 569
              ||||||:::       :::   ||||||::::::||||||||||||||||||||||
Db        160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179

Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA--------------------GGCCAT 608
              ||||||||||||||||||   ||||||:::                        |||
Db        180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199

Qy        609 AAT---------------------------------------------------------- 611
              |||
Db        200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219

Qy        612 --------------------------------CGAATGTGGAGAAAGAACCGTTCTTTC 638
                                             ||||||||||||||||||||||||
Db        220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239

Qy        639 TATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGG 698
                 |||:::   ||||||||||||||||||||   ||||||           |||
Db        240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258

Qy        699 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG 758
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Db        259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278

Qy        759 TCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAA 818
              ||||||   |||   ||||||||   :::|||:::|||   ::::::|||   ||||||
Db        279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298

Qy        819 GCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGA 878
              |||||||||:::   ||||||||||||||   ::::::   ||||||   ||||||
Db        299 AlaTyrIleThrPheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318

Qy        879 AGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATT 938
                      :::|||::::::|||      ||||||      |||      |||:::
Db        319 LysLeuProProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338

Qy        939 GACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTA 998
                    |||         |||||||||   :::|||      :::   |||:::|||
Db        339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357

Qy        999 GCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTAC---- 1054
                  |||         ||||||:::||||||||||||||||||:::::::|||
Db        358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377

Qy       1055 ----------------------------------------------ATCAAACCCACC 1066
                                                            ||||||||||||
Db        378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397

Qy       1067 TGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAAT 1120
              |||:::|||         :::|||      ||||||   ::::::::::|||
Db        398 CysLysGluThrMetLeuSerValLysPheIleAlaLysTyrIleLeuLysAsn 415

RESULT 8
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:

;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-7

Alignment Scores:
Pred. No.:                1.14e-63      Length:          417
Score:                    655.00        Matches:         150
Percent Similarity:       51.67%        Conservative:    66
Best Local Similarity:    35.89%        Mismatches:      138
Query Match:              23.59%        Indels:          65
DB:                       1             Gaps:            9

US-09-980-881A-1 (1-1573) x US-08-277-540-7 (1-417)

Qy          33 CTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCGTTCCAGAGT 92
               :::||||||:::         :::                 |||         |||
Db           7 MetAlaValIleTyrThrThrLeuAlaIleAlaProValHis---------PheAspArg 23

Qy          93 GGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAATCTT 152
                 :::|||            :::     :::          ||||||:::||||||
Db          24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43

Qy         153 ACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAA 212
               |||   :::   |||:::      |||   |||                  |||
Db          44 ThrGlnSerIleGluLeuAspPheTrpTyrProAspAlaIleHisAspIleAlaValAsn 63

Qy         213 AAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTAAAT 272
                  |||   |||   |||:::      :::          :::::::::   |||
Db          64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83

Qy         273 GTGAGCGGAATTCCATGCAGTGTCTTGCAGGCAGACGTGGAAGATCTTATTCAACAGCAG 332
                     |||         :::|||:::   |||:::::::::   |||::::::|||
Db          84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluGluIleGluLysGln 103

Qy         333 ATTTCC---AACGACACAGTCAGCCCCCAGCCTCCGCATCGTACTATGAACAGTATCAC 389
                        |||   ::::::   | |   |||          |||   :::|||:::
Db         104 PheAspValLysAspGluIleAlaGlyArgHisSer---------TyrAlaLysTyrAsn 120

Qy         390 TCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTT 449
                  ::::::|||   ||||||   |||   :::   |||:::||||||:::|||:::
Db         121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140

Qy         450 ACAAAAATCCACATTGGATCCTCATTTGAAGAAGTACCCACTCTATGTTTTAAAGGTTTCT 509
               ::::::|||   |||||||||:::   |||      ||||||||||||||||:::
Db         141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159

Qy         510 GGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAA 569
               ||||||:::         :::   ||||||::::::||||||||||||||||||||||
Db         160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179

Qy         570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA--------------------GGCCAT 608
               ||||||||||||||||||||   ||||||:::                    |||
Db         180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199

Qy         609 AAT---------------------------------------------------------- 611
               |||
Db         200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219

Qy         612 --------------------------------CGAATGTGGAGAAAGAACCGTTCTTTC 638
                                               |||||||||||||||||||||||||
Db         220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239

Qy         639 TATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGG 698
                  |||:::   ||||||||||||||||||||   ||||||            |||
Db         240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258

Qy         699 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG 758
                              ::::::      |||         |||   |||      ||||||
Db         259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278

Qy         759 TCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAA 818
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Db        279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298

Qy        819 GCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGA 878
Db        299 AlaTyrIleThrPheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318

Qy        879 AGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATT 938
Db        319 LysLeuProProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338

Qy        939 GACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTA 998
Db        339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357

Qy        999 GCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTAC---- 1054
Db        358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377

Qy       1055 ----------------------------------------------ATCAAACCCACC 1066
Db        378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397

Qy       1067 TGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAAT 1120
Db        398 CysLysGluThrMetLeuSerValLysPheIleAlaLysTyrIleLeuLysAsn 415

RESULT 9
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
;   APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;   TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/430,787A
;     FILING DATE:  27-APR-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/277,540
;     FILING DATE:  19-JUL-1994
;     APPLICATION NUMBER:  08/167727
;     FILING DATE:  15-DEC-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/959944
;     FILING DATE:  14-OCT-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/649591
;     FILING DATE:  01-FEB-91
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Hasak, Janet E.
;     REGISTRATION NUMBER:  28,616
;     REFERENCE/DOCKET NUMBER:  689D1C1D1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1896
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
; INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  417 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
US-08-430-787A-7

Alignment Scores:
Pred. No.:              1.14e-63      Length:          417
Score:                  655.00        Matches:         150
Percent Similarity:     51.67%        Conservative:    66
Best Local Similarity:  35.89%        Mismatches:      138
Query Match:            23.59%        Indels:          65
DB:                     1             Gaps:            9

US-09-980-881A-1 (1-1573) x US-08-430-787A-7 (1-417)

Qy         33 CTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCGTTCCAGAGT 92
Db          7 MetAlaValIleTyrThrThrLeuAlaIleAlaProValHis---------PheAspArg 23

Qy         93 GGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAATCTT 152
Db         24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43

Qy        153 ACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAA 212
Db         44 ThrGlnSerIleGluLeuAspPheTrpTyrProAspAlaIleHisAspIleAlaValAsn 63

Qy        213 AAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTAAAT 272
Db         64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83

Qy        273 GTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATTCAACAGCAG 332
Db         84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluGluIleGluLysGln 103

Qy        333 ATTTCC---AACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAGTATCAC 389
Db        104 PheAspValLysAspGluIleAlaGlyArgHisSer---------TyrAlaLysTyrAsn 120

Qy        390 TCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTT 449
Db        121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140

Qy        450 ACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAGGTTTCT 509
Db        141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159

Qy        510 GGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAA 569
Db        160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179

Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA----------GGCCAT 608
Db        180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199

Qy        609 AAT---------- 611
Db        200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219

Qy        612 ----------CGAATGTGGAGAAAGAACCGTTCTTTC 638
Db        220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239

Qy        639 TATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGG 698
Db        240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258

Qy        699 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG 758
Db        259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278

Qy        759 TCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAA 818
Db        279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298
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Qy        819 GCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGA 878
              |||||||||:::  ||||||||||||||   ::::::  ||||||  ||||||
Db        299 AlaTyrIleThrPheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318

Qy        879 AGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATT 938
                     :::|||::::::|||      ||||||      |||      |||:::
Db        319 LysLeuProProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338

Qy        939 GACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTA 998
                  |||        |||||||||   :::|||      :::   |||:::|||
Db        339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357

Qy        999 GCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTAC---- 1054
                  |||        ||||||:::||||||||||||||||||:::::|||
Db        358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377

Qy       1055 ----------------------------------------------ATCAAACCCACC 1066
                                                            ||||||||||||
Db        378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397

Qy       1067 TGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAAT 1120
              |||:::|||        :::|||      ||||||   ::::::::::::|||
Db        398 CysLysGluThrMetLeuSerValLysPheIleAlaLysTyrIleLeuLysAsn 415

RESULT 10
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  415 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-860-882A-57
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Alignment Scores:
Pred. No.:                2.78e-63      Length:          415
Score:                    651.50        Matches:         142
Percent Similarity:       52.03%        Conservative:    76
Best Local Similarity:    33.89%        Mismatches:      140
Query Match:              23.46%        Indels:          62
DB:                       2             Gaps:            8

US-09-980-881A-1 (1-1573) x US-08-860-882A-57 (1-415)

Qy         33 CTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCG---TTCCAG 89
              |||  |||||||||  :::  |||           |||           |||:::
Db          2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGluHisPheGlu 21

Qy         90 AGTGGCCAAGTTCTAGCTGCTCTTCCTACAACCTCTAGGCAAGTTCAAGTTCTACAGAAT 149
                 :::|||                          :::   :::::::::
Db         22 GlyGluLysValPheArgValAsnValGluAspGluAsnHisIleAsnIleIleArgGlu 41

Qy        150 CTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAG 209
              |||  :::|||  :::|||      |||:::|||  :::          |||
Db         42 LeuAlaSerThrThrGlnIleAspPheTrpLysProAspSerValThrGlnIleLysPro 61

Qy        210 AAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTA 269
                  |||  |||  |||  |||  |||         |||:::      |||
Db         62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81

Qy        270 AATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATTCAACAG 329
                 :::  :::         ||||||:::::::::::  ::::::::::::
Db         82 LysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101

Qy        330 CAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAGTATCAC 389
              |||      :::              ||||||:::      ||||||:::|||:::
Db        102 GlnPheAspSerArgVal---------ArgAlaThrGlyHisSerTyrGluLysTyrAsn 118

Qy        390 TCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTT 449
                  |||  :::|||  :::  :::        :::|||  ::::::
Db        119 LysTrpGluThrIleGluAlaTrpThrGlnGlnValAlaThrGluAsnProAlaLeuIle 138

Qy        450 ACAAAAATCCACATTGGATCCTCATTTGAAGAAGTACCCACTCTATGTTTTAAAGGTTTCT 509
              ::::::      ||||||::::::||||||         :::|||:::|||||||||
Db        139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeuLysVal--- 157

Qy        510 GGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAA 569
              ||||||        |||   ||||||::::::|||||||||   ||||||||||||
Db        158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177

Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA---------------------------- 602
              ||||||||||||||||||||  ||||||:::
Db        178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrGlyArg 197

Qy        602 ------------------------------------------------------------ 602

Db        198 GluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuProValLeuAsn 217

Qy        603 ------GGCCAT-----------------AATCGAATGTGGAGAAAGAACCGTTCTTTC 638
                    |||:::                 :::|||   |||||||||   ||||||
Db        218 IleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237

Qy        639 TATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGG 698
              :::      :::   ||||||||||||||   |||   ||||||                |||
Db        238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256

Qy        699 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG 758
              ||||||   |||||||||   :::   |||   ||||||||||||||||          |||
Db        257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyProAlaAlaGlu 276

Qy        759 TCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAA 818
              ||||||   |||   ||||||:::|||   |||:::|||      ::::::   ||||||
Db        277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296

Qy        819 GCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGA 878
              ||||||:::::::::|||||||||||||||   :::::::::||||||||||||
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```
Db        297 AlaTyrLeuThrIleHisSerTyrSerGlnMetMetIleTyrProTyrSerTyrAlaTyr 316

Qy        879 AGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATT 938
                  :::::::::   ||||||:::   :::|||       |||:::   :::
Db        317 LysLeuGlyGluAsnAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336

Qy        939 GACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTA 998
                 :::         |||:::||||||:::|||   |||:::   |||:::|||
Db        337 ---AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrThrIleTyrPro 355

Qy        999 GCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACATC- 1057
                |||.  ||||||   |||||||||   ||||||   ||||||:::|||||||||||
Db        356 AlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleArgTyrSerPheThrPhe 375

Qy       1058 ----------------------------------------------------AAACCCACC 1066
                                                                    :::   |||
Db        376 GluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIleArgAlaThr 395

Qy       1067 TGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTT 1123
                |||  |||  |||  |||:::      :::|||  :::|||:::  ::::::
Db        396 CysGluGluThrPheLeuAlaIleLysTyrValAlaSerTyrValLeuGluHisLeu 414

RESULT 11
US-09-011-769A-39
; Sequence 39, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;  INFORMATION FOR SEQ ID NO: 39:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 415 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39

Alignment Scores:
Pred. No.:              2.78e-63        Length:         415

Score:                  651.50          Matches:        142
Percent Similarity:     52.03%          Conservative:   76
Best Local Similarity:  33.89%          Mismatches:     140
Query Match:            23.46%          Indels:         62
DB:                     4               Gaps:           8

US-09-980-881A-1 (1-1573) x US-09-011-769A-39 (1-415)

Qy         33 CTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCG---TTCCAG 89
              |||  |||||||||  :::  |||          |||           |||:::
Db          2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGluHisPheGlu 21

Qy         90 AGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAAT 149
                 :::|||                          :::   :::::::::
Db         22 GlyGluLysValPheArgValAsnValGluAspGluAsnHisIleAsnIleIleArgGlu 41

Qy        150 CTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAG 209
              |||  :::|||  :::|||     |||:::|||  :::         |||
Db         42 LeuAlaSerThrThrGlnIleAspPheTrpLysProAspSerValThrGlnIleLysPro 61

Qy        210 AAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTA 269
                  |||  |||  |||  |||  |||        |||:::     |||
Db         62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81

Qy        270 AATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATTCAACAG 329
                 :::  :::         |||||:::::::::::  ::::::::::::
Db         82 LysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101

Qy        330 CAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAGTATCAC 389
              |||     :::              |||||:::        |||||:::|||:::
Db        102 GlnPheAspSerArgVal---------ArgAlaThrGlyHisSerTyrGluLysTyrAsn 118

Qy        390 TCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTT 449
                   |||   :::|||  :::  :::       :::|||   ::::::
Db        119 LysTrpGluThrIleGluAlaTrpThrGlnGlnValAlaThrGluAsnProAlaLeuIle 138

Qy        450 ACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAGGTTTCT 509
              ::::::      ||||||:::::||||||         :::|||:::|||||||||
Db        139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeuLysVal--- 157

Qy        510 GGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAA 569
              ||||||             |||  ||||||::::::|||||||||  ||||||||||||
Db        158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177

Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA-------------------------- 602
              ||||||||||||||||||||   ||||||:::
Db        178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrGlyArg 197

Qy        602 ------------------------------------------------------------ 602

Db        198 GluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuProValLeuAsn 217

Qy        603 ------GGCCAT-----------------AATCGAATGTGGAGAAAGAACCGTTCTTTC 638
                    |||:::                 :::|||  |||||||||  ||||||
Db        218 IleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237

Qy        639 TATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGG 698
              :::      :::  ||||||||||||||  |||  ||||||           |||
Db        238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256

Qy        699 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG 758
              ||||||  |||||||||  :::  |||  ||||||||||||||          |||
Db        257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyProAlaAlaGlu 276

Qy        759 TCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAA 818
              ||||||  |||  ||||||:::|||  |||:::|||      ::::::  ||||||
Db        277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296

Qy        819 GCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGA 878
              ||||||:::::::::|||||||||||||||  :::::::::|||||||||||
Db        297 AlaTyrLeuThrIleHisSerTyrSerGlnMetMetIleTyrProTyrSerTyrAlaTyr 316

Qy        879 AGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATT 938
```

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                    :::::::::   ||||||:::   :::|||         |||:::   :::
Db        317 LysLeuGlyGluAsnAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336

Qy        939 GACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTA 998
                  :::       |||:::||||||:::|||   |||:::   |||:::|||
Db        337 ---AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrThrIleTyrPro 355

Qy        999 GCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACATC- 1057
              |||   ||||||   |||||||||   ||||||   ||||||:::||||||||||||
Db        356 AlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleArgTyrSerPheThrPhe 375

Qy       1058 ----------------------------------------------------AAACCCACC 1066
                                                                  :::   |||
Db        376 GluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIleArgAlaThr 395

Qy       1067 TGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTT 1123
              |||   |||   |||   |||:::      :::|||   :::|||:::   ::::::
Db        396 CysGluGluThrPheLeuAlaIleLysTyrValAlaSerTyrValLeuGluHisLeu 414

RESULT 12
US-07-649-591B-6
; Sequence 6, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-6

Alignment Scores:
Pred. No.:              7.76e-63        Length:         417
Score:                  647.50          Matches:        143
Percent Similarity:     52.46%          Conservative:   81
Best Local Similarity:  33.49%          Mismatches:     132
Query Match:            23.32%          Indels:         72
DB:                     1               Gaps:           10

US-09-980-881A-1 (1-1573) x US-07-649-591B-6 (1-417)

Qy          6 ATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGT 65
                :::   ||||||:::         :::||||||:::      |||:::

Db          5 LeuProValGlyLeuIleAlaThrThrLeuAlaIle---AlaProVal---------- 19

Qy         66 GAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCT 125
                                |||         :::|||             |||:::
Db         20 --------------ArgPheAspArgGluLysValPheArgValLysProGlnAspGlu 34

Qy        126 AGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCG 185
              :::|||      :::::::::::|||       |||   |||:::      |||   |||
Db         35 LysGlnAlaAspIleIleLysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrPro 54

Qy        186 GTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGAT 245
                        :::                 |||   |||   |||:::      :::
Db         55 GlyAlaThrHisHisValAlaAlaAsnMetMetValAspPheArgValSerGluLysGlu 74

Qy        246 GTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCA 305
                  :::::::::   |||:::   :::   :::         :::|||:::
Db         75 SerGlnAlaIleGlnSerAlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHis 94

Qy        306 GACGTGGAAGATCTTATTCAACAGCAGATTTCC---AACGACACAGTCAGCCCCCGAGCC 362
              |||:::::::::   |||:::::|||            :::   :::      |||
Db         95 AspLeuGlnGluGluIleGluLysGlnPheAspValLysGluAspIleProGlyArgHis 114

Qy        363 TCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTT 422
              |||         |||   :::|||:::::      :::|||   :::|||   |||
Db        115 Ser---------TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLys 131

Qy        423 ATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAG 482
                  :::   :::::::::|||:::|||::::::::::|||   |||||||||:::   |||
Db        132 MetMetAspLysTyrProGluMetValSerArgIleLysIleGlySerThrValGluAsp 151

Qy        483 TACCCACTCTATGTTTTAAAGGTTTCTGCAAAAGAACAAACAGCCAAAAATGCCATATGG 542
                |||||||||||||||||:::   |||::::::          :::   ||||||:::
Db        152 AsnProLeuTyrValLeuLysIle---GlyGluLysAsnGluArgArgLysAlaIlePhe 170

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
              :::|||||||||||||||||||||||||:::|||||||||||||||   ||||||:::
Db        171 MetAspCysGlyIleHisAlaArgGluTrpValSerProAlaPheCysGlnTrpPheVal 190

Qy        602 ---------------------------------------------------------- 602

Db        191 TyrGlnAlaThrLysThrTyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMet 210

Qy        603 ---------------------------------GGCCAT-----------------AAT 611
                                              |||:::                 |||
Db        211 AsnPheTyrIleLeuProValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsn 230

Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
              |||||||||||||||||||||||          |||:::   |||||||||||||||||
Db        231 ArgMetTrpArgLysAsnArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeu 250

Qy        672 AATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
              |||   ||||||   :::       |||                 ::::::      |||:::
Db        251 AsnArgAsnPhe---AsnAlaSerTrpAsnSerIleProAsnThrAsnAspProCysAla 269

Qy        732 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 791
              :::   |||   |||       ||||||||||||   |||   |||||||||   :::|||
Db        270 AspAsnTyrArgGlySerAlaProGluSerGluLysGluThrLysAlaValThrAsnPhe 289

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851
              :::|||   ::::::|||:::||||||   ||||||:::   ||||||||||||||
Db        290 IleArgSerHisLeuAsnGluIleLysValTyrIleThrPheHisSerTyrSerGlnMet 309

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911
              ::::::|||||||||   ||||||                :::|||||:::|||:::
Db        310 LeuLeuProTyrGlyTyrThrSerLysLeuProProAsnHisGluAspLeuAlaLys 329

Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971
              ||||||                :::       |||         |||||||||   :::
Db        330 ValAlaLysIleGlyThrAspValLeu---SerThrArgTyrGluThrArgTyrIleTyr 348

Qy        972 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1031
              |||         |||:::|||         |||         ||||||   ||||||
Db        349 GlyProIleGluSerThrIleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAsp 368
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Qy       1032 TTGGGCATCAAATATTCGTTTAC---------------------------------- 1054
              ||||||||||||:::::|||
Db        369 LeuGlyIleLysHisThrPheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeu 388

Qy       1055 --------------ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
                           ||||||||||||||||||||        ||||||      |||
Db        389 LeuProGluSerArgIleLysProThrCysArgGluThrMetLeuAlaValLysPheIle 408

Qy       1100 GCTTGGCATGTCATTAGGAAT 1120
              |||   ::::::::::::::
Db        409 AlaLysTyrIleLeuLysHis 415

RESULT 13
US-08-277-540-6
; Sequence 6, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-6

Alignment Scores:
Pred. No.:              7.76e-63        Length:         417
Score:                  647.50          Matches:        143
Percent Similarity:     52.46%          Conservative:   81
Best Local Similarity:  33.49%          Mismatches:     132
Query Match:            23.32%          Indels:         72
DB:                     1               Gaps:           10

US-09-980-881A-1 (1-1573) x US-08-277-540-6 (1-417)

Qy          6 ATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGT 65
                ::   ||||||:::         :::|||||||:::      |||:::

Db          5 LeuProValGlyLeuIleAlaThrThrLeuAlaIle---AlaProVal---------- 19

Qy         66 GAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCT 125
                                  |||         :::|||         |||:::
Db         20 --------------ArgPheAspArgGluLysValPheArgValLysProGlnAspGlu 34

Qy        126 AGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCG 185
               :::|||      ::::::::::::|||      |||   |||:::      |||   |||
Db         35 LysGlnAlaAspIleIleLysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrPro 54

Qy        186 GTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGAT 245
                        :::                |||   |||   |||:::      :::
Db         55 GlyAlaThrHisHisValAlaAlaAsnMetMetValAspPheArgValSerGluLysGlu 74

Qy        246 GTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCA 305
                    :::::::::   |||:::   :::   :::          :::|||:::
Db         75 SerGlnAlaIleGlnSerAlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHis 94

Qy        306 GACGTGGAAGATCTTATTCAACAGCAGATTTCC---AACGACACAGTCAGCCCCCGAGCC 362
               |||:::::::::   |||::::::|||            :::   :::       |||
Db         95 AspLeuGlnGluGluIleGluLysGlnPheAspValLysGluAspIleProGlyArgHis 114

Qy        363 TCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTT 422
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Db        115 Ser---------TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLys 131

Qy        423 ATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAG 482
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Qy        483 TACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGG 542
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Db        152 AsnProLeuTyrValLeuLysIle---GlyGluLysAsnGluArgArgLysAlaIlePhe 170

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
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Qy        602 ------------------------------------------------------------ 602

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Qy        603 --------------------------------GGCCAT------------------AAT 611
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Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
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Db        270 AspAsnTyrArgGlySerAlaProGluSerGluLysGluThrLysAlaValThrAsnPhe 289

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851
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Db        290 IleArgSerHisLeuAsnGluIleLysValTyrIleThrPheHisSerTyrSerGlnMet 309

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911
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Db        310 LeuLeuProTyrGlyTyrThrSerLysLeuProProAsnHisGluAspLeuAlaLys 329

Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971
               ||||||                :::      |||         |||||||||   :::
Db        330 ValAlaLysIleGlyThrAspValLeu---SerThrArgTyrGluThrArgTyrIleTyr 348

Qy        972 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1031
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Qy       1032 TTGGGCATCAAATATTCGTTTAC---------------------------------- 1054
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Qy       1055 ---------------ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
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Qy       1100 GCTTGGCATGTCATTAGGAAT 1120
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Db        409 AlaLysTyrIleLeuLysHis 415
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RESULT 14
US-08-430-787A-6
; Sequence 6, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: 'patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-430-787A-6

Alignment Scores:

Pred. No.:	7.76e-63	Length:	417
Score:	647.50	Matches:	143
Percent Similarity:	52.46%	Conservative:	81
Best Local Similarity:	33.49%	Mismatches:	132
Query Match:	23.32%	Indels:	72
DB:	1	Gaps:	10

US-09-980-881A-1 (1-1573) x US-08-430-787A-6 (1-417)

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Qy         66 GAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCT 125
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Db         20 --------------ArgPheAspArgGluLysValPheArgValLysProGlnAspGlu 34

Qy        126 AGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCG 185
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Db         55 GlyAlaThrHisHisValAlaAlaAsnMetMetValAspPheArgValSerGluLysGlu 74

Qy        246 GTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCA 305
                    :::::::::    |||:::   :::   :::          :::|||:::
Db         75 SerGlnAlaIleGlnSerAlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHis 94

Qy        306 GACGTGGAAGATCTTATTCAACAGCAGATTTCC---AACGACACAGTCAGCCCCCGAGCC 362
              |||:::::::::   |||::::::|||            :::   :::      |||
Db         95 AspLeuGlnGluGluIleGluLysGlnPheAspValLysGluAspIleProGlyArgHis 114

Qy        363 TCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTT 422
              |||         |||   :::|||::::::      :::|||   :::|||   |||
Db        115 Ser---------TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLys 131

Qy        423 ATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAG 482
              :::   :::::::::|||:::|||:::::::::|||   |||||||||:::   |||
Db        132 MetMetAspLysTyrProGluMetValSerArgIleLysIleGlySerThrValGluAsp 151

Qy        483 TACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGG 542
              ||||||||||||||||||:::   |||::::::         :::   ||||||:::
Db        152 AsnProLeuTyrValLeuLysIle---GlyGluLysAsnGluArgArgLysAlaIlePhe 170

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
              :::|||||||||||||||||||||||||:::|||||||||||||||   ||||||:::
Db        171 MetAspCysGlyIleHisAlaArgGluTrpValSerProAlaPheCysGlnTrpPheVal 190

Qy        602 ------------------------------------------------------------ 602

Db        191 TyrGlnAlaThrLysThrTyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMet 210

Qy        603 --------------------------------GGCCAT----------------AAT 611
                                             |||:::                |||
Db        211 AsnPheTyrIleLeuProValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsn 230

Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
              ||||||||||||||||||||||||          |||:::   ||||||||||||||||
Db        231 ArgMetTrpArgLysAsnArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeu 250

Qy        672 AATAGCAACTTTGTCTCCAAACACTGGCGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
              |||   ||||||   :::      |||                 ::::::      |||:::
Db        251 AsnArgAsnPhe---AsnAlaSerTrpAsnSerIleProAsnThrAsnAspProCysAla 269

Qy        732 GAAACCTACTGTGGACTTTATCCTGAGACAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 791
              :::   |||   |||      ||||||||||||   |||   |||||||||   :::|||
Db        270 AspAsnTyrArgGlySerAlaProGluSerGluLysGluThrLysAlaValThrAsnPhe 289

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851
              :::|||   ::::::|||:::||||||   ||||||:::   ||||||||||||||
Db        290 IleArgSerHisLeuAsnGluIleLysValTyrIleThrPheHisSerTyrSerGlnMet 309

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911
              ::::::|||||||||   ||||||                ::::||||||:::|||:::
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Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971
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Db        349 GlyProIleGluSerThrIleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAsp 368

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Qy       1055 --------------ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
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RESULT 15
US-09-917-254-66
; Sequence 66, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George
;  APPLICANT:  Baak, Jan
;  TITLE OF INVENTION: Prognostic Classification of Breast Cancer
;  FILE REFERENCE: B0801/7224(JRV)
;  CURRENT APPLICATION NUMBER: US/09/917,254
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: US 60/222,093
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-917-254-66

Alignment Scores:
Pred. No.:              7.76e-63        Length:         417
Score:                  647.50          Matches:        143
Percent Similarity:     52.46%          Conservative:   81
Best Local Similarity:  33.49%          Mismatches:     132
Query Match:            23.32%          Indels:         72
DB:                     4               Gaps:           10

US-09-980-881A-1 (1-1573) x US-09-917-254-66 (1-417)

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Qy         66 GAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCT 125
Db         20 --------------ArgPheAspArgGluLysValPheArgValLysProGlnAspGlu 34

Qy        126 AGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCG 185
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Qy        186 GTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGAT 245
Db         55 GlyAlaThrHisHisValAlaAlaAsnMetMetValAspPheArgValSerGluLysGlu 74

Qy        246 GTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCA 305
Db         75 SerGlnAlaIleGlnSerAlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHis 94

Qy        306 GACGTGGAAGATCTTATTCAACAGCAGATTTCC---AACGACACAGTCAGCCCCCGAGCC 362
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Qy        363 TCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTT 422
Db        115 Ser---------TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLys 131

Qy        423 ATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAG 482
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Qy        483 TACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGG 542
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Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
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Qy       1055 --------------ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
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Qy       1100 GCTTGGCATGTCATTAGGAAT 1120
Db        409 AlaLysTyrIleLeuLysHis 415

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Job time : 64.5 secs
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 2741442

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	68.5	1902.5	68.5	386	14	US-10-212-877-2	Sequence 2, Appli
3	67.9	1885	67.9	423	14	US-10-379-836-17	Sequence 17, Appl
4	67.5	1874	67.5	423	9	US-09-813-133A-4	Sequence 4, Appli
5	67.5	1874	67.5	423	14	US-10-212-877-4	Sequence 4, Appli
6	67.0	1861.5	67.0	428	15	US-10-115-479-68	Sequence 68, Appl
7	67.0	1861.5	67.0	428	15	US-10-115-479-70	Sequence 70, Appl
8	64.7	1796	64.7	423	14	US-10-379-836-2	Sequence 2, Appli
9	57.3	1592.5	57.3	422	14	US-10-379-836-18	Sequence 18, Appl
10	56.5	1568.5	56.5	422	14	US-10-379-836-16	Sequence 16, Appl
11	53.7	1492.5	53.7	322	15	US-10-115-479-64	Sequence 64, Appl
12	52.1	1446.5	52.1	354	15	US-10-115-479-66	Sequence 66, Appl
13	32.0	889	32.0	211	9	US-09-925-302-467	Sequence 467, App
14	32.0	889	32.0	211	10	US-09-925-302-467	Sequence 467, App
15	23.5	652.5	23.5	417	15	US-10-074-978A-267	Sequence 267, App
16	23.5	652.5	23.5	417	15	US-10-074-978A-268	Sequence 268, App
17	23.5	652.5	23.5	417	16	US-10-477-515-3	Sequence 3, Appli
18	23.3	647.5	23.3	417	14	US-10-229-546-2	Sequence 2, Appli
19	23.3	647.5	23.3	417	14	US-10-229-546-9	Sequence 9, Appli
20	23.3	647.5	23.3	417	14	US-10-341-434-188	Sequence 188, App
21	23.3	647.5	23.3	417	15	US-10-262-511-72	Sequence 72, Appl
22	23.3	646	23.3	416	15	US-10-074-978A-269	Sequence 269, App
23	23.2	644	23.2	402	14	US-10-379-836-20	Sequence 20, Appl
24	23.1	640.5	23.1	416	15	US-10-074-978A-270	Sequence 270, App
25	22.9	635.5	22.9	437	13	US-10-200-344-10	Sequence 10, Appl
26	22.9	635.5	22.9	437	14	US-10-274-639-12	Sequence 12, Appl
27	22.9	635.5	22.9	437	15	US-10-333-574-12	Sequence 12, Appl
28	22.8	634.5	22.8	716	9	US-09-910-059-125	Sequence 125, App
29	22.8	634	22.8	416	15	US-10-074-978A-266	Sequence 266, App
30	22.8	633.5	22.8	437	17	US-10-757-262-128	Sequence 128, App
31	22.7	630.5	22.7	434	16	US-10-477-515-2	Sequence 2, Appli
32	20.6	571.5	20.6	613	9	US-09-910-059-113	Sequence 113, App
33	20.6	571.5	20.6	613	16	US-10-608-710-4	Sequence 4, Appli
34	20.5	570	20.5	374	9	US-09-888-615-61	Sequence 61, Appl
35	20.3	563	20.3	444	14	US-10-176-306-74	Sequence 74, Appl
36	19.7	546.5	19.7	399	14	US-10-200-910-8	Sequence 8, Appli
37	19.7	546.5	19.7	399	17	US-10-843-130-8	Sequence 8, Appli
38	19.3	536.5	19.3	286	16	US-10-408-765A-1959	Sequence 1959, Ap
39	19.3	536	19.3	419	15	US-10-072-012-788	Sequence 788, App
40	19.1	529.5	19.1	350	13	US-10-200-344-12	Sequence 12, Appl
41	18.8	522	18.8	286	15	US-10-072-012-887	Sequence 887, App
42	18.7	520	18.7	419	15	US-10-257-174-40	Sequence 40, Appl
43	18.7	520	18.7	436	14	US-10-200-910-6	Sequence 6, Appli
44	18.7	520	18.7	436	15	US-10-072-012-784	Sequence 784, App
45	18.7	520	18.7	436	15	US-10-257-174-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Alignment Scores:
Pred. No.: 9.61e-186 Length: 386

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Score:                  1902.50         Matches:        363
Percent Similarity:     94.30%          Conservative:   1
Best Local Similarity:  94.04%          Mismatches:     5
Query Match:            68.51%          Indels:         18
DB:                     9               Gaps:           1

US-09-980-881A-1 (1-1573) x US-09-813-133A-2 (1-386)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200

Qy        618 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGC 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220

Qy        678 AACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 737
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240

Qy        738 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260

Qy        798 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280

Qy        858 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300

Qy        918 AGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCAT 977
              ||||||||||||||||||||:::|||  ||||||||||||||||||||||||||||||||
Db        301 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 320

Qy        978 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340

Qy       1038 ATCAAATATTCGTT---------------------------------------------- 1051
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Db        341 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 360

Qy       1052 ------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGG 1105
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrp 380

Qy       1106 CATGTCATTAGGAATGTT 1123
              ||||||||||||||||||
Db        381 HisValIleArgAsnVal 386

RESULT 2
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-212-877-2

Alignment Scores:
Pred. No.:              9.61e-186       Length:         386
Score:                  1902.50         Matches:        363
Percent Similarity:     94.30%          Conservative:   1
Best Local Similarity:  94.04%          Mismatches:     5
Query Match:            68.51%          Indels:         18
DB:                     14              Gaps:           1

US-09-980-881A-1 (1-1573) x US-10-212-877-2 (1-386)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
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Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200

Qy        618 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGC 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220

Qy        678 AACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 737
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240

Qy        738 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 797
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260

Qy        798 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 857
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280

Qy        858 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 917
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300

Qy        918 AGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCAT 977
              |||:|||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db        301 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 320

Qy        978 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340

Qy       1038 ATCAAATATTCGTT---------------------------------------------- 1051
              ||||||||||||
Db        341 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 360

Qy       1052 ------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGG 1105
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrp 380

Qy       1106 CATGTCATTAGGAATGTT 1123
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Db        381 HisValIleArgAsnVal 386

RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Homo sapiens

US-10-379-836-17

Alignment Scores:
Pred. No.:                6.17e-184      Length:          423
Score:                    1885.00        Matches:         365
Percent Similarity:       86.52%         Conservative:    1
Best Local Similarity:    86.29%         Mismatches:      3
Query Match:              67.88%         Indels:          55
DB:                       14             Gaps:            2

US-09-980-881A-1 (1-1573) x US-10-379-836-17 (1-423)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
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Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              |||||||||||||||||||||||||||||||||||||||||||||||||||         
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy        608 ------------------------------------------------------------ 608

Db        201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db        221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||    
Db        241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
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Db        301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
                ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT----------------------------------------------------TAC 1054
                |||                                                    |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
                |||||||||
Db        421 ArgAsnVal 423

RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

Alignment Scores:
Pred. No.:              8.28e-183       Length:         423
Score:                  1874.00         Matches:        363
Percent Similarity:     86.05%          Conservative:   1
Best Local Similarity:  85.82%          Mismatches:     5
Query Match:            67.48%          Indels:         55
DB:                     9               Gaps:           2

US-09-980-881A-1 (1-1573) x US-09-813-133A-4 (1-423)

Qy          18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy          78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy         138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy         198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy         258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy         318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy         378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy         438 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 497
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy         498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
                ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db         161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy         558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy         608 ------------------------------------------------------------ 608

Db         201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy         609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                       ||||||||||||||||||
Db         221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy         627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
                |||||||||||||||||||||||||||||| ||||||||||||||||||   ||||||
Db         241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy         687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
                |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy         747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
                |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy         807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy         867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy         927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
                ||||||||||||:::|||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db         341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy         987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy        1047 TCGTT----------------------------------------------------TAC 1054
                |||                                                    |||
Db         381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy        1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy        1115 AGGAATGTT 1123
                |||||||||
Db         421 ArgAsnVal 423

RESULT 5
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```
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-10-212-877-4

Alignment Scores:
Pred. No.:              8.28e-183       Length:         423
Score:                  1874.00         Matches:        363
Percent Similarity:     86.05%          Conservative:   1
Best Local Similarity:  85.82%          Mismatches:     5
Query Match:            67.48%          Indels:         55
DB:                     14              Gaps:           2

US-09-980-881A-1 (1-1573) x US-10-212-877-4 (1-423)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200

Qy        608 ------------------------------------------------------------ 608

Db        201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db        221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              ||||||||||||:::|||   ||||||||||||||||||||||||||||||||||||||
Db        341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT----------------------------------------------------TAC 1054
              |||                                                    |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
              |||||||||
Db        421 ArgAsnVal 423

RESULT 6
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
```

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;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-115-479-68

Alignment Scores:
Pred. No.:                1.59e-181      Length:          428
Score:                    1861.50        Matches:         363
Percent Similarity:       85.05%         Conservative:    1
Best Local Similarity:    84.81%         Mismatches:      5
Query Match:              67.03%         Indels:          60
DB:                       15             Gaps:            3

US-09-980-881A-1 (1-1573) x US-10-115-479-68 (1-428)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAG--------------GTTTCTGCAAAAGAACAAACAGCCAAAAATGCCATATGG 542
              ||||||              ||||||||||||||||||  ||||||||||||||||||
Db        161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATCGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200

Qy        603 GGCCAT---------------------------------------------------------- 608
              ||||||
Db        201 GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuVal 220

Qy        609 ----------------------------------------------------------AAT 611
                                                                        |||
Db        221 AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsn 240

Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260

Qy        672 AATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 280

Qy        732 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 791
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        281 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 300

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 320

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 340

Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db        341 ValAlaSerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHis 360

Qy        972 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 380

Qy       1032 TTGGGCATCAAATATTCGTT---------------------------------------- 1051
              ||||||||||||||||||||
Db        381 LeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeu 400

Qy       1052 ------------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
                         ||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIle 420

Qy       1100 GCTTGGCATGTCATTAGGAATGTT 1123
              |||||||||||||||||||||||||
Db        421 AlaTrpHisValIleArgAsnVal 428

RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
```

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;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-70

Alignment Scores:
Pred. No.:              1.59e-181      Length:         428
Score:                  1861.50        Matches:        363
Percent Similarity:     85.05%         Conservative:   1
Best Local Similarity:  84.81%         Mismatches:     5
Query Match:            67.03%         Indels:         60
DB:                     15             Gaps:           3

US-09-980-881A-1 (1-1573) x US-10-115-479-70 (1-428)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAG--------------GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGG 542
              ||||||              ||||||||||||||||||   ||||||||||||||||||
Db        161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200

Qy        603 GGCCAT---------------------------------------------------- 608
              ||||||
Db        201 GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuVal 220

Qy        609 ----------------------------------------------------------AAT 611
                                                                        |||
Db        221 AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsn 240

Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260

Qy        672 AATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 280

Qy        732 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 300

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 320

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 340

Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db        341 ValAlaSerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHis 360

Qy        972 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 380

Qy       1032 TTGGGCATCAAATATTCGTT---------------------------------------- 1051
              ||||||||||||||||||||
Db        381 LeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeu 400

Qy       1052 ------------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
                         ||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIle 420
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Qy       1100 GCTTGGCATGTCATTAGGAATGTT 1123
              ||||||||||||||||||||||||
Db        421 AlaTrpHisValIleArgAsnVal 428

RESULT 8
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Papio hamadryas
US-10-379-836-2

Alignment Scores:
Pred. No.:              8.26e-175     Length:          423
Score:                  1796.00       Matches:         347
Percent Similarity:     84.16%        Conservative:    9
Best Local Similarity:  82.03%        Mismatches:      13
Query Match:            64.67%        Indels:          55
DB:                     14            Gaps:            2

US-09-980-881A-1 (1-1573) x US-10-379-836-2 (1-423)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||   ||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         61 LeuIleGluLysLysLysGlnValHisPhePheValAsnSerSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||::::::
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluLeuIleThrGluLysTyr 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||:::||||||:::||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerTyrGluLysHisProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaMetTrpIleAspCysGlyIle 180

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGlu 200

Qy        608 ------------------------------------------------------------ 608

Db        201 TyrTyrGlyIleIleGlyGluTyrThrAsnLeuLeuArgHisValAspPheTyrValMet 220

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db        221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTCCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        241 AsnArgSerPheTyrAlaAsnAsnArgCysIleGlyThrAspLeuAsnArgAsnPheAla 260

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        261 SerLysHisTrpCysGluGluGlyAlaSerSerPheSerCysSerGluThrTyrCysGly 280

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||   |||||||||:::||||||||||||||||||||
Db        281 LeuTyrProGluSerGluProGluAlaLysAlaValAlaAsnPheLeuArgArgAsnIle 300

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AsnHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              ||||||||||||  ||||||||||||||  ||||||||||||||  |||||||||
Db        341 ValArgAlaIleGlnLysThrSerLysAsnIleArgTyrThrHisGlyArgGlySerGlu 360

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        361 ThrLeuTyrLeuAlaProGlyGlyAlaAspAspTrpIleTyrAspLeuGlyIleLysTyr 380

Qy       1047 TCGTT-------------------------------------------------------TAC 1054
              |||                                                       |||
Db        381 SerPheThrIleGluLeuArgAspThrGlyLysTyrGlyPheLeuLeuProGluArgTyr 400

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||:::::::||||||||||||||||||||||||||||||||||||||
Db        401 IleLysProThrCysLysAspAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420

Qy       1115 AGGAATGTT 1123
              |||||||||
Db        421 ArgAsnVal 423

RESULT 9
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-379-836-18

Alignment Scores:
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Pred. No.:	6.09e-154	Length:	422
Score:	1592.50	Matches:	309
Percent Similarity:	79.15%	Conservative:	25
Best Local Similarity:	73.22%	Mismatches:	33
Query Match:	57.35%	Indels:	56
DB:	14	Gaps:	3

US-09-980-881A-1 (1-1573) x US-10-379-836-18 (1-422)

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Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              |||||||||      |||   :::||||||   |||:::|||:::   |||||||||
Db          1 MetLysLeuHisGlyLeuGlyIleLeuValAlaIleIleLeuTyr---GluGlnHisGly 19

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db         20 PheAlaPheGlnSerGlyGlnValLeuSerAlaLeuProArgThrSerArgGlnValGln 39

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              :::|||||||||||||||||||||||||:::|||||||||||||||||||||||||:::
Db         40 LeuLeuGlnAsnLeuThrThrThrTyrGluValValLeuTrpGlnProValThrAlaGlu 59

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
                 |||   |||||||||:::|||||||||||||||||||||||||||||||:::|||
Db         60 PheIleGluLysLysLysGluValHisPhePheValAsnAlaSerAspValAspSerVal 79

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||   ||||||   :::||||||:::   :::|||||||||
Db         80 LysAlaHisLeuAsnValSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              |||||:::||||||      ||||||||||||||||||||||||||||||||||||||
Db        100 LeuIleGluGlnGlnThrPheAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 119

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              |||||||||||||||||||||||||||||||||||||||||   |||||||||:::|||
Db        120 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluValIleThrGluGlnHis 139

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              |||||||||||   ||||||:::||||||||||||||||||||||||||||||||||||
Db        140 ProAspMetLeuGlnLysIleTyrIleGlySerSerPheGluLysTyrProLeuTyrVal 159

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              ||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        160 LeuLysValSerGlyLysGluGlnArgIleLysAsnAlaIleTrpIleAspCysGlyIle 179

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        180 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyTyrValThrGln 199

Qy        608 ------------------------------------------------------------ 608

Db        200 PheHisGlyLysGluAsnLeuTyrThrArgLeuLeuArgHisValAspPheTyrIleMet 219

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db        220 ProValMetAsnValAspGlyTyrAspTyrThrTrpLysLysAsnArgMetTrpArgLys 239

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              |||||||||   :::   ||||||   |||:::|||||||||||||||   ||||||
Db        240 AsnArgSerAlaHisLysAsnAsnArgCysValGlyThrAspLeuAsnArgAsnPheAla 259

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        260 SerLysHisTrpCysGluLysGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 279

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgArgAsnIle 299

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              :::   |||||||||||||||||||||||||||||||||||||||   |||:::|||||||||
Db        300 AspHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnGlnIleLeuPheProTyr 319

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 SerTyrAsnArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 339

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              |||||||||||:::      :::|||||||||||||||||||||||||   |||||||||
Db        340 ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              :::|||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        360 SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleLysTyr 379

Qy       1047 TCGTT----------------------------------------------------TAC 1054
              |||                                                    |||
Db        380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgTyr 399

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              |||||||||||||||   ||||||   ||||||:::|||||||||   ||||||||||||
Db        400 IleLysProThrCysAlaGluAlaLeuAlaAlaIleSerLysIleValTrpHisValIle 419

Qy       1115 AGGAAT 1120
              ||||||
Db        420 ArgAsn 421
```

RESULT 10
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Alignment Scores:			
Pred. No.:	1.76e-151	Length:	422
Score:	1568.50	Matches:	305
Percent Similarity:	78.44%	Conservative:	26
Best Local Similarity:	72.27%	Mismatches:	36
Query Match:	56.48%	Indels:	56
DB:	14	Gaps:	3

US-09-980-881A-1 (1-1573) x US-10-379-836-16 (1-422)

```
Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              |||||||||      |||   |||||||||   |||:::|||:::   |||:::|||
Db          1 MetLysLeuTyrGlyLeuGlyValLeuValAlaIleIleLeuTyr---GluLysHisGly 19

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
                 |||||||||||||||   ||||||:::|||||||||||||||||||||||||||||||
Db         20 LeuAlaPheGlnSerGlyHisValLeuSerAlaLeuProArgThrSerArgGlnValGln 39

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              :::|||||||||||||||||||||||||:::|||||||||||||||||||||||||:::
Db         40 LeuLeuGlnAsnLeuThrThrThrTyrGluValValLeuTrpGlnProValThrAlaGlu 59

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
                 |||   |||||||||:::|||||||||||||||||||||||||||||:::::|||
Db         60 PheIleGluLysLysLysGluValHisPhePheValAsnAlaSerAspValAsnSerVal 79

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||:::||||||   |||   ||||||   :::|||||||:::   :::|||||||||
```

```
Db        80 LysAlaTyrLeuAsnAlaSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99

Qy       318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
             ||||||||||||||||   ||||||||||||||||||||||||||||:::|||||||||
Db       100 LeuIleGlnGlnGlnThrSerAsnAspThrValSerProArgAlaSerSerSerTyrTyr 119

Qy       378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
             ||||||||||||||||||||||||||||||||||||||||   |||||||||:::|||
Db       120 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluValIleThrGluGlnHis 139

Qy       438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
             ||||||||||||   ||||||:::|||||||||||||:::|||||||||||||||||||||
Db       140 ProAspMetLeuGlnLysIleTyrIleGlySerSerTyrGluLysTyrProLeuTyrVal 159

Qy       498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
             ||||||||||||||||||||         ||||||||||||||||||||||||||||||
Db       160 LeuLysValSerGlyLysGluHisArgValLysAsnAlaIleTrpIleAspCysGlyIle 179

Qy       558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
             |||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       180 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyTyrValThrGln 199

Qy       608 ------------------------------------------------------------ 608

Db       200 PheHisGlyLysGluAsnThrTyrThrArgLeuLeuArgHisValAspPheTyrIleMet 219

Qy       609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                     ||||||||||||||||||
Db       220 ProValMetAsnValAspGlyTyrAspTyrThrTrpLysLysAsnArgMetTrpArgLys 239

Qy       627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
             |||||||||   :::   ||||||   |||:::|||||||||||||||   ||||||
Db       240 AsnArgSerValHisMetAsnAsnArgCysValGlyThrAspLeuAsnArgAsnPheAla 259

Qy       687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
             ||||||||||||||||||:::|||||||||||   |||||||||||||||||||||||||
Db       260 SerLysHisTrpCysGluLysGlyAlaSerSerPheSerCysSerGluThrTyrCysGly 279

Qy       747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
             ||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db       280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgArgAsnIle 299

Qy       807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
             |||   |||||||||||||||||||||||||||||||||   |||:::|||||||||
Db       300 AsnHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnGlnIleLeuPheProTyr 319

Qy       867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
             ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       320 SerTyrAsnArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 339

Qy       927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
             ||||||||||||:::      :::|||||||||||||||||||||||   |||||||||
Db       340 ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359

Qy       987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
             :::||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db       360 SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleLysTyr 379

Qy      1047 TCGTTTACATC---------------------------------------------------- 1057
             |||||||||
Db       380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgPhe 399

Qy      1058 ---AAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
                ||||||||||||   ||||||   ||||||||||||||||||||||||||||||||||
Db       400 IleLysProThrCysAlaGluAlaLeuAlaAlaValSerLysIleAlaTrpHisValIle 419

Qy      1115 AGGAAT 1120
             ||||||
Db       420 ArgAsn 421

RESULT 11
US-10-115-479-64
; Sequence 64, Application US/10115479

; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-64

Alignment Scores:
Pred. No.:              1e-143          Length:         322
Score:                  1492.50         Matches:        301
Percent Similarity:     78.24%          Conservative:   1
Best Local Similarity:  77.98%          Mismatches:     3
Query Match:            53.75%          Indels:         82
DB:                     15              Gaps:           2

US-09-980-881A-1 (1-1573) x US-10-115-479-64 (1-322)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTCTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              |||||||||||||||||||||||   |||||||||||||||||||||||
Db        161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAsp--------- 177

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 617

Db        177 ------------------------------------------------------------ 177

Qy        618 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGC 677

Db        177 ------------------------------------------------------------ 177

Qy        678 AACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 737

Db        177 ------------------------------------------------------------ 177

Qy        738 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 797
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 ---CysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 196

Qy        798 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 216

Qy        858 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 236

Qy        918 AGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCAT 977
              ||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db        237 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 256

Qy        978 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 276

Qy       1038 ATCAAATATTCGTT---------------------------------------------- 1051
              ||||||||||||
Db        277 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 296

Qy       1052 ------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGG 1105
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrp 316
```

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Qy       1106 CATGTCATTAGGAATGTT 1123
              ||||||||||||||||||
Db        317 HisValIleArgAsnVal 322

RESULT 12
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-66

Alignment Scores:
Pred. No.:              5.39e-139       Length:         354
Score:                  1446.50         Matches:        291
Percent Similarity:     67.99%          Conservative:   0
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Best Local Similarity:  67.99%          Mismatches:     4
Query Match:            52.09%          Indels:         134
DB:                     15              Gaps:           4

US-09-980-881A-1 (1-1573) x US-10-115-479-66 (1-354)

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Qy        498 TTAAAG--------------GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGG 542
              ||||||              ||||||||||||||||||   ||||||||||||||||||
Db        161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180

Qy        543 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200

Qy        603 GGCCAT------------------------------------------------------ 608
              ||||||
Db        201 GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuVal 220

Qy        609 ----------------------------------------------------------AAT 611
                                                                        |||
Db        221 AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsn 240

Qy        612 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260

Qy        672 AATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
              |||   ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 280

Qy        732 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 791
              ||||||||||||||||||||||||||
Db        281 GluThrTyrCysGlyLeuTyrProGlu---------------------------------- 289

Qy        792 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 851

Db        289 ------------------------------------------------------------ 289

Qy        852 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 911

Db        289 ------------------------------------------------------------ 289
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Qy        912 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACAT 971

Db        289 ------------------------------------------------------------ 289

Qy        972 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1031
                                                                ||||||||||||
Db        290 ---------SerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 306

Qy       1032 TTGGGCATCAAATATTCGTT---------------------------------------- 1051
              ||||||||||||||||||
Db        307 LeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeu 326

Qy       1052 ------------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATA 1099
                         ||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 LeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLysIle 346

Qy       1100 GCTTGGCATGTCATTAGGAATGTT 1123
              |||||||||||||||||||||||||
Db        347 AlaTrpHisValIleArgAsnVal 354
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RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05910
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.:              6.74e-82        Length:         211
Score:                  889.00          Matches:        173
Percent Similarity:     83.33%          Conservative:   2
Best Local Similarity:  82.38%          Mismatches:     9
Query Match:            32.01%          Indels:         27
DB:                     9               Gaps:           3

US-09-980-881A-1 (1-1573) x US-09-925-302-467 (1-211)

Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA----------------------GGC 605
              |||||||||          |||   |||   :::
Db          3 TrpIleSer---MetLeuCysArgTrpLeuMetTrpMetValMetAsnTyrSerTrpLys 21

Qy        606 CATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACA 665
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThr 41

Qy        666 GACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCA 725
              |||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||||
Db         42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSer 61

Qy        726 TGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCT 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAla 81

Qy        786 AGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCC 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 SerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSer 101
```

```
Qy        846 CAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTG 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121

Qy        906 TCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTAT 965
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyr 141

Qy        966 ACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATC 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161

Qy       1026 TATGATTTGGGCATCAAATATTCGTT---------------------------------- 1051
              ||||||||||||||||||||||||||
Db        162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGly 181

Qy       1052 ------------------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCT 1093
                                   ||||||||||||||||||||||||||||||||||||||||||
Db        182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSer 201

Qy       1094 AAAATAGCTTGGCATGTCATTAGGAATGTT 1123
              |||||||||||||||||||||||||||||
Db        202 LysIleAlaTrpHisValIleArgAsnVal 211
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RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:

Pred. No.:	6.74e-82	Length:	211
Score:	889.00	Matches:	173
Percent Similarity:	83.33%	Conservative:	2
Best Local Similarity:	82.38%	Mismatches:	9
Query Match:	32.01%	Indels:	27
DB:	10	Gaps:	3

US-09-980-881A-1 (1-1573) x US-09-925-302-467 (1-211)

```
Qy        570 TGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA-----------------------GGC 605
              |||||||||        |||   |||   :::
Db          3 TrpIleSer---MetLeuCysArgTrpLeuMetTrpMetValMetAsnTyrSerTrpLys 21

Qy        606 CATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACA 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThr 41

Qy        666 GACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCA 725
              |||||||||    ||||||   ||||||||||||||||||||||||||||||||||||
Db         42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSer 61

Qy        726 TGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCT 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAla 81

Qy        786 AGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCC 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 SerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSer 101

Qy        846 CAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTG 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121

Qy        906 TCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTAT 965
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyr 141

Qy        966 ACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATC 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161

Qy       1026 TATGATTTGGGCATCAAATATTCGTT---------------------------------- 1051
              ||||||||||||||||||||||||||
Db        162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGly 181

Qy       1052 ------------------TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCT 1093
                                   ||||||||||||||||||||||||||||||||||||||||||
Db        182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSer 201

Qy       1094 AAAATAGCTTGGCATGTCATTAGGAATGTT 1123
              |||||||||||||||||||||||||||||
Db        202 LysIleAlaTrpHisValIleArgAsnVal 211
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RESULT 15
US-10-074-978A-267
; Sequence 267, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284

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;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 267
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-267

Alignment Scores:
Pred. No.:                1.5e-57        Length:          417
Score:                    652.50         Matches:         142
Percent Similarity:       52.13%         Conservative:    78
Best Local Similarity:    33.65%         Mismatches:      141
Query Match:              23.50%         Indels:          62
DB:                       15             Gaps:            8

US-09-980-881A-1 (1-1573) x US-10-074-978A-267 (1-417)

Qy         24 CTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTCTTCGCG 83
              :::   :::|||   |||||||||   :::   |||           |||
Db          1 MetLeuAlaLeuLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGlu 20

Qy         84 ---TTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTT 140
                 |||:::      :::|||                                 :::   :::
Db         21 HisPheGluGlyGluLysValPheArgValAsnValGluAspGluAsnHisIleAsnIle 40

Qy        141 CTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTT 200
              ::::::   |||   :::|||   :::|||      |||:::|||   :::
Db         41 IleArgGluLeuAlaSerThrThrGlnIleAspPheTrpLysProAspSerValThrGln 60

Qy        201 ATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAA 260
              |||              |||   |||   |||   |||   |||           |||:::
Db         61 IleLysProHisSerThrValAspPheArgValLysAlaGluAspThrValThrValGlu 80

Qy        261 GCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTT 320
                 |||      :::   :::         ||||||:::::::::::::   ::::::
Db         81 AsnValLeuLysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnVal 100

Qy        321 ATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAA 380
              ::::::   |||      :::                 ||||||:::          ||||||
Db        101 ValGluAlaGlnPheAspSerArgVal---------ArgAlaThrGlyHisSerTyrGlu 117

Qy        381 CAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCT 440
              :::|||:::           |||   :::|||   :::   :::         :::|||
Db        118 LysTyrAsnLysTrpGluThrIleGluAlaTrpThrGlnGlnValAlaThrGluAsnPro 137

Qy        441 GATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTA 500
                 ::::::::::::      ||||||:::::|||||         :::|||:::|||
Db        138 AlaLeuIleSerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeu 157

Qy        501 AAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCAT 560
              ||||||   ||||||            |||   ||||||::::::|||||||||   |||
Db        158 LysVal---GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHis 176

Qy        561 GCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA------------------ 602
              ||||||||||||||||||||||||||||||   ||||||:::
Db        177 AlaArgGluTrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThr 196

Qy        602 ---------------------------------------------------------- 602

Db        197 TyrGlyArgGluIleGlnValThrGluLeuAspLysLeuAspPheTyrValLeuPro 216

Qy        603 --------------GGCCAT-----------------AATCGAATGTGGAGAAAGAAC 629
                           |||:::                 :::|||   |||||||||
Db        217 ValLeuAsnIleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThr 236

Qy        630 CGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCC 689
              ||||||   :::      :::   |||||||||||||||   |||   ||||||
Db        237 ArgSerThrHisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---Asp 255

Qy        690 AAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTT 749
                    |||||||||   |||||||||   :::   |||   |||||||||||||||
Db        256 AlaGlyTrpCysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyPro 275

Qy        750 TATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAAC 809
                    |||||||||   |||   |||||:::|||   |||:::|||      ::::::
Db        276 AlaAlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSer 295

Qy        810 CAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCC 869
                 ||||||||||:::::::::|||||||||||||||   :::::::::|||||||||
Db        296 SerIleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetMetIleTyrProTyrSer 315

Qy        870 TATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTT 929
                 |||                 :::::::::   ||||||:::   :::|||      |||
Db        316 TyrAlaTyrLysLeuGlyGluAsnAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrVal 335

Qy        930 CGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACC 989
              :::   :::      :::         |||:::||||||:::|||   |||:::   |||
Db        336 LysGluLeu---AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrThr 354

Qy        990 TTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCG 1049
              :::|||   |||   ||||||   |||||||||   ||||||   ||||||:::||||||
Db        355 IleTyrProAlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleArgTyrSer 374

Qy       1050 TTTACATC---------------------------------------------------- 1057
              ||||||
Db        375 PheThrPheGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIle 394

Qy       1058 AAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGG 1117
              :::   ||||||   |||   |||   |||:::      :::|||   :::|||:::
Db        395 ArgAlaThrCysGluGluThrPheLeuAlaIleLysTyrValAlaSerTyrValLeuGlu 414

Qy       1118 AATGTT 1123
              ::::::
Db        415 HisLeu 416


Search completed: October 28, 2004, 19:28:11
Job time : 226.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 22:52:22 ; Search time 151 Seconds
(without alignments)
7404.443 Million cell updates/sec

Title: US-09-980-881A-1
Perfect score: 1573
Sequence: 1 agaaaattgctgttgggatg.....aaaaaaaaaaaaaaaaaaa 1573

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1469.8	93.4	1625	4	US-09-813-133A-1	Sequence 1, Appli
2	1372	87.2	1749	1	US-07-649-591B-2	Sequence 2, Appli
3	1372	87.2	1749	1	US-08-277-540-2	Sequence 2, Appli
4	1372	87.2	1749	1	US-08-430-787A-2	Sequence 2, Appli
5	918	58.4	1272	2	US-08-869-057-1	Sequence 1, Appli
6	478.6	30.4	55827	4	US-09-813-133A-3	Sequence 3, Appli
7	124	7.9	927	2	US-08-782-760-5	Sequence 5, Appli
8	124	7.9	927	5	PCT-US96-00995-5	Sequence 5, Appli
9	123.4	7.8	921	1	US-08-696-139-3	Sequence 3, Appli
10	123.4	7.8	1215	1	US-08-696-139-1	Sequence 1, Appli
11	109	6.9	1263	4	US-09-011-769A-38	Sequence 38, Appl
12	107.6	6.8	1622	4	US-09-023-655-1020	Sequence 1020, Ap
13	107.4	6.8	999	2	US-08-860-882A-67	Sequence 67, Appl
14	107.4	6.8	999	4	US-09-011-769A-50	Sequence 50, Appl
15	107.4	6.8	1053	2	US-08-860-882A-64	Sequence 64, Appl
16	107.4	6.8	1053	4	US-09-011-769A-46	Sequence 46, Appl
17	107.4	6.8	1263	2	US-08-860-882A-56	Sequence 56, Appl
18	107.4	6.8	1284	2	US-08-860-882A-71	Sequence 71, Appl
19	107.4	6.8	1284	4	US-09-011-769A-55	Sequence 55, Appl
20	104.2	6.6	1053	4	US-09-463-451-27	Sequence 27, Appl
c 21	104.2	6.6	1053	4	US-09-463-451-28	Sequence 28, Appl
22	104.2	6.6	1059	2	US-08-860-882A-74	Sequence 74, Appl
23	104.2	6.6	1059	2	US-08-860-882A-77	Sequence 77, Appl
24	104.2	6.6	1059	4	US-09-011-769A-59	Sequence 59, Appl
25	104.2	6.6	1059	4	US-09-011-769A-63	Sequence 63, Appl
26	101	6.4	1870	3	US-09-171-945-112	Sequence 112, App
27	101	6.4	2154	3	US-09-171-945-124	Sequence 124, App
28	92.8	5.9	1311	4	US-09-675-305-9	Sequence 9, Appli
29	92.8	5.9	1311	4	US-10-200-344-9	Sequence 9, Appli
30	92.8	5.9	2128	4	US-09-675-305-13	Sequence 13, Appl
31	92.8	5.9	2128	4	US-10-200-344-13	Sequence 13, Appl
32	88.6	5.6	1050	4	US-09-675-305-11	Sequence 11, Appl
33	88.6	5.6	1050	4	US-10-200-344-11	Sequence 11, Appl
34	87.6	5.6	1200	4	US-09-710-099-7	Sequence 7, Appli
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36	83.6	5.3	945	4	US-09-710-099-3	Sequence 3, Appli
37	83.6	5.3	945	4	US-09-710-099-11	Sequence 11, Appl
38	83.6	5.3	945	4	US-10-200-910-3	Sequence 3, Appli
39	83.6	5.3	945	4	US-10-200-910-11	Sequence 11, Appl
40	82.4	5.2	359	4	US-09-513-999C-3571	Sequence 3571, Ap
41	78.4	5.0	741	4	US-09-675-305-5	Sequence 5, Appli
42	78.4	5.0	741	4	US-10-200-344-5	Sequence 5, Appli
43	71.6	4.6	1251	3	US-08-640-906-3	Sequence 3, Appli
44	71.6	4.6	1251	3	US-09-395-936-3	Sequence 3, Appli
45	70.6	4.5	1257	3	US-08-640-906-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Query Match 93.4%; Score 1469.8; DB 4; Length 1625;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1553; Conservative 0; Mismatches 17; Indels 53; Gaps 2;

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Qy          2 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 60

Qy         62 CTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 121
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 CTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 120

Qy        122 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 180

Qy        182 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATC 240

Qy        242 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 300

Qy        302 GGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 361
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGATGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 360

Qy        362 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 420

Qy        422 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 480

Qy        482 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATG 541
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        481 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATG 540

Qy        542 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 600

Qy        602 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 660

Qy        662 AACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 721
              |||||||||||||||  |||||||  ||||||||||||||||||||||||||||||||||
Db        661 AACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 720

Qy        722 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 780

Qy        782 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 840

Qy        842 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 900

Qy        902 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAG 961
              |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db        901 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAG 960

Qy        962 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTG 1020

Qy       1022 GATCTATGATTTGGGCATCAAATATTCGT------------------------------ 1050
              |||||||||||||||||||||||||||||
Db       1021 GATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATA 1080

Qy       1051 ---------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1089
                                   ||||||||||||||||||||||||||||||||||||||
Db       1081 CGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1140

Qy       1090 CTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGC 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGC 1200

Qy       1150 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1260

Qy       1210 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1320

Qy       1270 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAA 1329
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1321 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAA 1379

Qy       1330 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1439

Qy       1390 AAGCAACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACG 1449
              |||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1440 AAGCAAGTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACG 1499

Qy       1450 CTGATCATTGGATCCTACTCAACAAAAGCAAGGGTGGTCAGAAGTACATTAAAGATTTCT 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1500 CTGATCATTGGATCCTACTCAACAAAAGCAAGGGTGGTCAGAAGTACATTAAAGATTTCT 1559

Qy       1510 GCTCCAAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAAAAAAA 1569
              |||||||||||||||||||||||| ||| | | || |||||||||| ||||||||||||
Db       1560 GCTCCAAATTTTCAATAAATTTCTGCTTCTGCCTTTAAAAAAAAAAATAAAAAAAAAAAA 1619

Qy       1570 AAA 1572
              | |
Db       1620 ATA 1622
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RESULT 2
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  hybridization probe
;      LOCATION:  133 to 178
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  potential clip site
;      LOCATION:  380 to 382
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  signal sequence
;      LOCATION:  41 to 106
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-07-649-591B-2

  Query Match             87.2%;  Score 1372;  DB 1;  Length 1749;
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  Best Local Similarity   90.3%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches    5;  Indels  163;  Gaps    2;

Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 83

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         84 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 143

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 203

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 263

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 323

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 383

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 443

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 503

Qy        481 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 563

Qy        541 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 623

Qy        601 TAGGCCAT---------------------------------------------------- 608
              ||||||||
Db        624 TAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTG 683

Qy        609 ----------------------------------------------------------A 609
                                                                         |
Db        684 TGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGA 743

Qy        610 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 803

Qy        670 TGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 729
              ||||||| |||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        804 TGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 863

Qy        730 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 923

Qy        790 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 983

Qy        850 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 1043

Qy        910 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACAC 969
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1044 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC 1103

Qy        970 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1163

Qy       1030 ATTTGGGCATCAAATATTCGT---------------------------------------- 1050
              |||||||||||||||||||||
Db       1164 ATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCT 1223

Qy       1051 ------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1097
                         ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 TGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

Qy       1098 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1343

Qy       1158 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1403

Qy       1218 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1463

Qy       1278 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1523

Qy       1338 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1583

Qy       1398 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1643

Qy       1458 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1703

Qy       1518 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAA 1563
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       1704 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAA 1749
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RESULT 3
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727

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;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-277-540-2

  Query Match             87.2%;  Score 1372;  DB 1;  Length 1749;
  Best Local Similarity   90.3%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches    5;  Indels  163;  Gaps    2;

Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 83

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         84 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 143

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 203

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 263

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 323

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 383

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 443

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 503

Qy        481 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 563

Qy        541 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 623

Qy        601 TAGGCCAT---------------------------------------------------- 608
              ||||||||
Db        624 TAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTG 683

Qy        609 ----------------------------------------------------------A 609
                                                                         |
```

```
Db        684 TGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGA 743

Qy        610 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 803

Qy        670 TGAATAGCAACTTTGTCTCCAAACACTGCTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 729
              ||||||| |||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        804 TGAATAGGAACTTTGCTTCCAAACACTGCTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 863

Qy        730 CGGAAACCTACTGTGGACTTTATCCTGACTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 CGGAAACCTACTGTGGACTTTATCCTGACTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 923

Qy        790 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 983

Qy        850 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 909
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        984 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 1043

Qy        910 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACAC 969
              |||||||||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db       1044 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC 1103

Qy        970 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1163

Qy       1030 ATTTGGGCATCAAATATTCGT---------------------------------------- 1050
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Db       1164 ATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCT 1223

Qy       1051 ------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1097
                         ||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 TGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

Qy       1098 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1343

Qy       1158 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1403

Qy       1218 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1463

Qy       1278 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1523

Qy       1338 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1583

Qy       1398 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1643

Qy       1458 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1703

Qy       1518 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAA 1563
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1704 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAA 1749
```

RESULT 4
US-08-430-787A-2

```
; Sequence 2, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-787A-2

  Query Match             87.2%;  Score 1372;  DB 1;  Length 1749;
  Best Local Similarity   90.3%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches    5;  Indels  163;  Gaps    2;

Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 83

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         84 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 143

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 203

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 263

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 323

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
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Db        324 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 383

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 443

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 503

Qy        481 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 563

Qy        541 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 623

Qy        601 TAGGCCAT---------------------------------------------------- 608
              ||||||||
Db        624 TAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTG 683

Qy        609 ----------------------------------------------------------A 609
                                                                         |
Db        684 TGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGA 743

Qy        610 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 803

Qy        670 TGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 729
              ||||||| |||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        804 TGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 863

Qy        730 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 923

Qy        790 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 983

Qy        850 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 1043

Qy        910 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACAC 969
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1044 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC 1103

Qy        970 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1163

Qy       1030 ATTTGGGCATCAAATATTCGT---------------------------------------- 1050
              |||||||||||||||||||
Db       1164 ATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCT 1223

Qy       1051 ------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1097
                         ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 TGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

Qy       1098 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1343

Qy       1158 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1403

Qy       1218 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1277
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Db       1404 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1463

Qy       1278 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1337
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1523

Qy       1338 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1397
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1583

Qy       1398 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1457
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Db       1584 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1643

Qy       1458 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1517
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1703

Qy       1518 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAAA 1563
                ||||||||||||||||||||||||||||||||||||||||||||||
Db       1704 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAAA 1749


RESULT 5
US-08-869-057-1
; Sequence 1, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    PUBLICATION INFORMATION:
;      AUTHORS:  Eaton, Dan L.
;      AUTHORS:  Malloy, Beth E.
;      AUTHORS:  Tsai, Siao P
;      AUTHORS:  Henzel, William
;      AUTHORS:  Drayna, Dennis
;      TITLE:  Isolation, Molecular Cloning, and Partial
;      TITLE:  Characterization of a No. 5985562el Carboxypeptidase B
;      TITLE:  from Human Plasma
;      JOURNAL:  J. Biol. Chem.
;      VOLUME:  266
;      ISSUE:  32
;      PAGES:  21833-21838
;      DATE:  No. 5985562 15-1991
US-08-869-057-1

  Query Match             58.4%;  Score 918;  DB 2;  Length 1272;
  Best Local Similarity   86.8%;  Pred. No. 8.2e-224;
  Matches 1104;  Conservative    0;  Mismatches    5;  Indels  163;  Gaps    2;

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 60

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 120

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 240

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 300

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 360

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 420

Qy        438 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 480

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
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Db        481 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 540

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 600

Qy        609 ------------------------------------------------------------ 608

Db        601 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 660

Qy        609 ----------------------------------------AATCGAATGTGGAGAAAG 626
                                                       ||||||||||||||||||
Db        661 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 720

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTCCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        721 AACCGTTCTTTCTATGCGAACAATCATTCCATCGGAACAGACCTGAATAGGAACTTTGCT 780

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 840

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 900

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 960

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
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Db        961 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1020

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1080

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1140

Qy       1047 TCGT----------------------------------------------------TTAC 1054
              ||||                                                    ||||
Db       1141 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1200

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1260

Qy       1115 AGGAATGTTTAA 1126
              ||||||||||||
Db       1261 AGGAATGTTTAA 1272
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RESULT 6
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 30.4%; Score 478.6; DB 4; Length 55827;
Best Local Similarity 98.0%; Pred. No. 1.9e-111;
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Qy       1051 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 1110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53334 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 53393

Qy       1111 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 1170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53394 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 53453

Qy       1171 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 1230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53454 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 53513

Qy       1231 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 1290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53514 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 53573

Qy       1291 GGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAAAAGTCTAGTTACC 1350
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      53574 GGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAAAATTGTAAAAGTCTAGTTACC 53632

Qy       1351 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 1410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53633 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 53692

Qy       1411 TAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCATTGGATCCTACTCA 1470
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      53693 TAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACGCTGATCATTGGATCCTACTCA 53752

Qy       1471 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 1530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53753 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 53812

Qy       1531 TCTTCTTCTCCTTTAAAAAAAAAAA 1555
              ||| ||| | | || | ||| | ||
Db      53813 TCTGCTTGTGCCTTTAGAAATACAA 53837
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RESULT 7
US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
; GENERAL INFORMATION:
; APPLICANT: Hartman, Jacob
; APPLICANT: Fulga, Netta
; APPLICANT: Mendelovitch, Simona
; APPLICANT: Gorecki, Marian
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
US-08-782-760-5

Query Match 7.9%; Score 124; DB 2; Length 927;
Best Local Similarity 57.9%; Pred. No. 5.3e-22;
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;

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Qy        613 GAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGA 672
              |||||||||||||| | ||| |||      ||    | |   ||| | ||   ||||| |
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Db        362 GAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGACCCCA 421

Qy        673 ATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGG 732

Db        422 ACAGGAATTTTAATGC---TGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478

Qy        733 AAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCT 792

Db        479 AAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGATTTCA 538

Qy        793 TGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATA 852

Db        539 TCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAGATGA 598

Qy        853 TAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAG 912

Db        599 TGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAATGCCC 658

Qy        913 TAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATG 972

Db        659 TGGTGAAAGGTGCGGCAAAGGAGCTTGCC---ACTCTGCATGGCACCAAGTACACATATG 715

Qy        973 GCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATT 1032

Db        716 GCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTATGATC 775

Qy       1033 TGGGCATCAAATATTCGTTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTC 1092

Db        776 AGGGAATCAAATATTCCTTTACCTTTGA-ACTCCGGGATACAGGCTTCTTTGGCTTTCTC 834


RESULT 8
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
;  GENERAL INFORMATION:
;    APPLICANT:  Bio-Technology General Corp.
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00995
;      FILING DATE:  25-JAN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847-A-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  927 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..927
PCT-US96-00995-5

  Query Match             7.9%;  Score 124;  DB 5;  Length 927;
  Best Local Similarity   57.9%;  Pred. No. 5.3e-22;
  Matches  278;  Conservative    0;  Mismatches  195;  Indels    7;  Gaps    3;

Qy        613 GAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGA 672

Db        362 GAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGACCCCA 421

Qy        673 ATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGG 732

Db        422 ACAGGAATTTTAATGC---TGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478

Qy        733 AAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCT 792

Db        479 AAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGATTTCA 538

Qy        793 TGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATA 852

Db        539 TCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAGATGA 598

Qy        853 TAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAG 912

Db        599 TGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAATGCCC 658

Qy        913 TAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATG 972

Db        659 TGGTGAAAGGTGCGGCAAAGGAGCTTGCC---ACTCTGCATGGCACCAAGTACACATATG 715

Qy        973 GCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATT 1032

Db        716 GCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTATGATC 775

Qy       1033 TGGGCATCAAATATTCGTTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTC 1092

Db        776 AGGGAATCAAATATTCCTTTACCTTTGA-ACTCCGGGATACAGGCTTCTTTGGCTTTCTC 834


RESULT 9
US-08-696-139-3
; Sequence 3, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..921
US-08-696-139-3

  Query Match             7.8%;  Score 123.4;  DB 1;  Length 921;
  Best Local Similarity   56.3%;  Pred. No. 7.5e-22;
  Matches  273;  Conservative    0;  Mismatches  206;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
              | ||  |  || |  || | | |    |     | | || ||||||||||||||||| |||
Db        321 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGAAAGACCCG 380

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
              |||  | ||||    | |   ||||| || |||||||  || || || ||||   |
Db        381 CTCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTTGATGCTGG 440

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
                |||||        || || || |    | | |||   || || |||||||||  |
Db        441 G---TGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGC 497

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
              | | ||||| |||  |||    |||||  |||||  |||  |  | |  ||  ||  |
Db        498 TGCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAACCTCTCCTC 557

Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
              || |||||||||  | |   || || ||||||||  |||   ||| | |  || |||||||||
Db        558 CATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCTTATTCCTA 617

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
              |      |       | |  || |||  ||  ||  |    | || |  |  || ||
Db        618 TGATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCTGCCGTGAA 677

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
              |   |||      ||     |    |||| ||| ||| | ||||  ||  |   |||  |
Db        678 AGAACTTG---CTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCTACAACAAT 734

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
              || |  ||| |||| ||    || || |||    |||||     || ||||||||||| ||
Db        735 CTATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAATATTCCTT 794

Qy       1052 TACAT 1056
              || |
Db        795 CACCT 799


RESULT 10
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1215 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1215
US-08-696-139-1

  Query Match             7.8%;  Score 123.4;  DB 1;  Length 1215;
  Best Local Similarity   56.3%;  Pred. No. 8.3e-22;
  Matches  273;  Conservative    0;  Mismatches  206;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
              | ||  |  || |  || | | |    |     | | || ||||||||||||||||| |||
Db        615 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGAAAGACCCG 674

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
              |||  | ||||    | |   ||||| || |||||||  || || || ||||   |
Db        675 CTCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTTGATGCTGG 734

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
                |||||        || || || |    | | |||   || || |||||||||  |
Db        735 G---TGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGC 791

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
              | | ||||| |||  |||    |||||  |||||  |||  |  | |  ||  ||  |
Db        792 TGCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAACCTCTCCTC 851

Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
              || |||||||||  | |   || || ||||||||  |||   ||| | |  || |||||||||
Db        852 CATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCTTATTCCTA 911

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
              |      |       | |  || |||  ||  ||  |    | || |  |  || ||
Db        912 TGATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCTGCCGTGAA 971

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
              |   |||      ||     |    |||| ||| ||| | ||||  ||  |   |||  |
Db        972 AGAACTTG---CTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCTACAACAAT 1028

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
              || |  ||| |||| ||    || || |||    |||||     || ||||||||||| ||
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Db       1029 CTATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAATATTCCTT 1088

Qy       1052 TACAT 1056
                 || |
Db       1089 CACCT 1093


RESULT 11
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 38:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1263 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

  Query Match             6.9%;  Score 109;  DB 4;  Length 1263;
  Best Local Similarity   54.4%;  Pred. No. 3.9e-18;
  Matches  264;  Conservative    0;  Mismatches  215;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
              | ||  |  || |  || | | |     |     | | |  ||| | ||||||||||  ||
Db        645 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCG 704

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
              ||   | || |     |   |||||| || ||||||| || || || ||||    |
Db        705 CTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTTGATGC--- 761

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
                  ||||||||    || || ||  |   | | ||    ||||| |||||||||| |
Db        762 TGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGC 821

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
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Db        822 CGCAGAGTCTGAAAAGGAAACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTC 881

Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
              ||  ||  |||||  |  |  ||  ||  ||  ||||||||     ||  |  |  ||  ||  ||  ||
Db        882 CATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATA 941

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGCAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
              | |  |      |  |  || |||  ||  ||  |    | || |  |   | ||
Db        942 TGCTTACAAACTCGGTGAGAACAATGCTCAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 1001

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
              |   ||| |    |     |    |||| ||| ||| ||||||  ||  |   |||  |
Db       1002 AGAACTTGCC---TCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAAT 1058

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
              ||  |  ||| |||| ||    |||||  ||  |||||    || |||| ||||||  ||
Db       1059 CTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 1118

Qy       1052 TACAT 1056
                 || |
Db       1119 CACCT 1123


RESULT 12
US-09-023-655-1020
; Sequence 1020, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1020:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1622 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g179933
US-09-023-655-1020
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  Query Match             6.8%;  Score 107.6;  DB 4;  Length 1622;
  Best Local Similarity   55.6%;  Pred. No. 9.7e-18;
  Matches  250;  Conservative    0;  Mismatches  194;  Indels    6;  Gaps    2;

Qy        607 ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAG 666
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Db        686 AGAACCGCATGTGGAGAAAAAATCGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTG 745

Qy        667 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCAT 726
              |||| || || || |||    |   |  |||         |    ||| |  | |||
Db        746 ACCTCAACAGGAATTTTAATGCTTCA---TGGAACTCCATTCCTAACACCAATGACCCAT 802

Qy        727 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTA 786
              |  | || | |||  | ||   |   || ||||| ||   |||   ||| || ||  |||
Db        803 GTGCAGATAACTATCGGGGCTCTGCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTA 862

Qy        787 GTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCC 846
              |||| | |||||  |  | ||  | || || |  |||||| | | |||| ||||||
Db        863 ATTTCATTAGAAGCCACCTGAATGAAATCAAGGTTTACATCACCTTCCATTCCTACTCCC 922

Qy        847 AGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGT 906
              ||    || ||||||| |||   |||||  ||          |||||||||  ||
Db        923 AGATGCTATTGTTTCCCTATGGATATACATCAAAACTGCCACCTAACCATGAGGACTTGG 982

Qy        907 CTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATA 966
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Db        983 CCAAAGTTGCAA---AGATTGGCACTGATGTTCTATCAACTCGATATGAAACCCGCTACA 1039

Qy        967 CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCT 1026
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Db       1040 TCTATGGCCCAATAGAATCAACAATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTT 1099

Qy       1027 ATGATTTGGGCATCAAATATTCGTTTACAT 1056
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Db       1100 ATGACCTGGGCATCAAACACACATTTGCCT 1129


RESULT 13
US-08-860-882A-67
; Sequence 67, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  999 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-67

  Query Match             6.8%;  Score 107.4;  DB 2;  Length 999;
  Best Local Similarity   54.2%;  Pred. No. 9e-18;
  Matches  263;  Conservative    0;  Mismatches  216;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
              | ||  |  || |  || | | |     |    | | |  ||| | ||||||||||  ||
Db        387 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCG 446

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
              ||   | || |      |   ||||| || |||||||  || || || ||||    |
Db        447 CTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTTGATGC--- 503

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
              ||||||||    || || ||  |   | | ||    |||| ||||||||||  |
Db        504 TGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGC 563

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
              | ||||| |||   ||    |||||  |||||  ||||  |  | |  ||  ||
Db        564 CGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTC 623

Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
              || || |||||  | |  || || || ||||||||    ||  | |  || || || ||
Db        624 CATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATA 683

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
              | |     |     |  |  || |||  ||  ||  |    | ||| |  |   | ||
Db        684 TGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 743

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
              |   ||| |   |    |   |||| ||| ||| ||||||  ||  |   |||  |
Db        744 AGAACTTGCC---TCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAAT 800

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
              || |  ||| |||| ||    |||||  |||    |||||     || |||| |||||| ||
Db        801 CTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 860

Qy       1052 TACAT 1056
              ||| |
Db        861 CACCT 865


RESULT 14
US-09-011-769A-50
; Sequence 50, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
```

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;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;    INFORMATION FOR SEQ ID NO: 50:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 999 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION: 1..987
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION: 67..987
;        SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-011-769A-50

  Query Match             6.8%;  Score 107.4;  DB 4;  Length 999;
  Best Local Similarity   54.2%;  Pred. No. 9e-18;
  Matches  263;  Conservative    0;  Mismatches  216;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
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Db        387 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCG 446

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
               ||   | || |       |   ||||| || ||||||| || || || ||||   |
Db        447 CTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTTGATGC--- 503

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
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Db        504 TGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGC 563

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
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Db        564 CGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTC 623

Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
               || || |||||  | |  || || || ||||||||    ||  | |  || || || ||
Db        624 CATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATA 683

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
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Db        684 TGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 743

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
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Db        744 AGAACTTGCC---TCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAAT 800

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
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Db        801 CTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 860

Qy       1052 TACAT 1056
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Db        861 CACCT 865


RESULT 15
US-08-860-882A-64
; Sequence 64, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1053 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-64

  Query Match             6.8%;  Score 107.4;  DB 2;  Length 1053;
  Best Local Similarity   54.2%;  Pred. No. 9.2e-18;
  Matches  263;  Conservative    0;  Mismatches  216;  Indels    6;  Gaps    2;

Qy        572 GATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
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Db        387 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCG 446

Qy        632 TTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 691
               ||   | || |       |   ||||| || ||||||| || || || ||||   |
Db        447 CTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTTGATGC--- 503

Qy        692 ACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 751
              ||||||||    || || ||  |   | | ||    ||||| |||||||||| |
Db        504 TGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGC 563

Qy        752 TCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCA 811
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Db        564 CGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTC 623
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Qy        812 GATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTA 871
              || || |||||  | |  || || || |||||||||    ||  | |  || || || ||
Db        624 CATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATA 683

Qy        872 TACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCG 931
              | |    |       |  |  || |||  ||  ||  |    | || |  |   | ||
Db        684 TGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 743

Qy        932 TGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTT 991
              |  ||| |   |     |    |||| ||| ||| ||||||  ||  |  |||  |
Db        744 AGAACTTGCC---TCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAAT 800

Qy        992 ATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTT 1051
              || |  ||| |||| ||    ||||| |||   |||||    || |||| ||||||  ||
Db        801 CTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 860

Qy       1052 TACAT 1056
              || |
Db        861 CACCT 865
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 23:58:17 ; Search time 809 Seconds
(without alignments)
9969.985 Million cell updates/sec

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Perfect score: 1573
Sequence: 1 agaaaattgctgttgggatg.....aaaaaaaaaaaaaaaaaaaa 1573

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1469.8	93.4	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1372	87.2	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1343.8	85.4	1743	16	US-10-115-479-67	Sequence 67, Appl
5	932.8	59.3	1344	16	US-10-115-479-69	Sequence 69, Appl
6	858.8	54.6	1272	15	US-10-379-836-1	Sequence 1, Appli
7	853.8	54.3	1400	9	US-09-925-302-24	Sequence 24, Appl
8	853.8	54.3	1400	10	US-09-925-302-24	Sequence 24, Appl
9	688	43.7	1037	16	US-10-115-479-63	Sequence 63, Appl
10	610.4	38.8	1132	16	US-10-115-479-65	Sequence 65, Appl
11	478.6	30.4	55827	9	US-09-813-133A-3	Sequence 3, Appli
12	478.6	30.4	55827	14	US-10-212-877-3	Sequence 3, Appli
13	331.2	21.1	416	9	US-09-960-352-14595	Sequence 14595, A
14	286.8	18.2	397	9	US-09-960-352-8425	Sequence 8425, Ap
c 15	137.2	8.7	431	9	US-09-917-800A-468	Sequence 468, App
16	131	8.3	1547	13	US-10-027-632-265133	Sequence 265133,
17	131	8.3	1547	13	US-10-027-632-265134	Sequence 265134,
18	131	8.3	1547	13	US-10-027-632-265135	Sequence 265135,
19	131	8.3	1547	13	US-10-027-632-265136	Sequence 265136,
20	131	8.3	1547	15	US-10-027-632-265133	Sequence 265133,
21	131	8.3	1547	15	US-10-027-632-265134	Sequence 265134,
22	131	8.3	1547	15	US-10-027-632-265135	Sequence 265135,
23	131	8.3	1547	15	US-10-027-632-265136	Sequence 265136,
24	107.6	6.8	1254	14	US-10-229-546-3	Sequence 3, Appli
25	107.6	6.8	1622	14	US-10-229-546-1	Sequence 1, Appli
26	107.6	6.8	1622	15	US-10-429-802-21	Sequence 21, Appl
27	107.6	6.8	1622	16	US-10-430-503-12	Sequence 12, Appl
28	107.6	6.8	1622	16	US-10-262-511-71	Sequence 71, Appl
29	107.6	6.8	1622	16	US-10-641-643-1020	Sequence 1020, Ap
30	107.6	6.8	1633	15	US-10-341-434-187	Sequence 187, App
31	107.6	6.8	1740	14	US-10-116-802-95	Sequence 95, Appl
32	104.8	6.7	473	16	US-10-242-535A-42160	Sequence 42160, A
33	104.8	6.7	473	16	US-10-085-783A-42160	Sequence 42160, A
34	101	6.4	1870	9	US-09-910-059-112	Sequence 112, App
35	101	6.4	1870	17	US-10-608-710-3	Sequence 3, Appli
36	101	6.4	2154	9	US-09-910-059-124	Sequence 124, App
37	94.6	6.0	1332	9	US-09-954-456-1141	Sequence 1141, Ap
38	92.8	5.9	1302	17	US-10-477-515-1	Sequence 1, Appli
39	92.8	5.9	1311	13	US-10-200-344-9	Sequence 9, Appli
40	92.8	5.9	1907	18	US-10-757-262-127	Sequence 127, App
41	92.8	5.9	1993	15	US-10-274-639-33	Sequence 33, Appl
42	92.8	5.9	1993	16	US-10-333-574-33	Sequence 33, Appl
43	92.8	5.9	2128	13	US-10-200-344-13	Sequence 13, Appl
44	91.6	5.8	936	15	US-10-106-698-1866	Sequence 1866, Ap
45	88.6	5.6	517	14	US-10-198-846-12472	Sequence 12472, A

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Query Match 93.4%; Score 1469.8; DB 9; Length 1625;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1553; Conservative 0; Mismatches 17; Indels 53; Gaps 2;

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Qy          2 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 61
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Db          1 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 60

Qy         62 CTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 121
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Db         61 CTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 120

Qy        122 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 181
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Db        121 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 180
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Qy       182 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCATC 241
Db       181 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCATC 240

Qy       242 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 301
Db       241 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 300

Qy       302 GGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 361
Db       301 GGCAGATGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 360

Qy       362 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 421
Db       361 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 420

Qy       422 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 481
Db       421 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 480

Qy       482 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATG 541
Db       481 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATG 540

Qy       542 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 601
Db       541 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 600

Qy       602 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 661
Db       601 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 660

Qy       662 AACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 721
Db       661 AACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 720

Qy       722 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 781
Db       721 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 780

Qy       782 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 841
Db       781 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 840

Qy       842 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 901
Db       841 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 900

Qy       902 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAG 961
Db       901 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAG 960

Qy       962 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTG 1021
Db       961 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTG 1020

Qy      1022 GATCTATGATTTGGGCATCAAATATTCGT------------------------------ 1050
Db      1021 GATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATA 1080

Qy      1051 --------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1089
Db      1081 CGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1140

Qy      1090 CTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGC 1149
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Qy      1150 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1209
Db      1201 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1260

Qy      1210 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1269
Db      1261 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1320

Qy      1270 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAA 1329
Db      1321 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAA 1379

Qy      1330 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1389
Db      1380 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1439

Qy      1390 AAGCAACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACG 1449
Db      1440 AAGCAAGTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACG 1499

Qy      1450 CTGATCATTGGATCCTACTCAACAAAAGCAAGGGTGGTCAGAAGTACATTAAAGATTTCT 1509
Db      1500 CTGATCATTGGATCCTACTCAACAAAAGCAAGGGTGGTCAGAAGTACATTAAAGATTTCT 1559

Qy      1510 GCTCCAAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAAAAAAAA 1569
Db      1560 GCTCCAAATTTTCAATAAATTTCTGCTTCTGCCTTTAAAAAAAAAAATAAAAAAAAAAAA 1619

Qy      1570 AAA 1572
Db      1620 ATA 1622
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RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Query Match 93.4%; Score 1469.8; DB 14; Length 1625;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1553; Conservative 0; Mismatches 17; Indels 53; Gaps 2;

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Qy          2 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 61
Db          1 GAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTT 60

Qy         62 CTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 121
Db         61 CTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAAC 120

Qy        122 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 181
Db        121 CTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCA 180

Qy        182 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCATC 241
Db        181 GCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCATC 240

Qy        242 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 301
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Db        241 TGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCT 300

Qy        302 GGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 361
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGATGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGC 360

Qy        362 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATT 420

Qy        422 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAA 480

Qy        482 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATG 541
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        481 GTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATG 540

Qy        542 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 601
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Db        541 GATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCAT 600

Qy        602 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 661
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Db        601 AGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGG 660

Qy        662 AACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 721
              |||||||||||||| |||||||  ||||||||||||||||||||||||||||||||||||
Db        661 AACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTC 720

Qy        722 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 781
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Db        721 CTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGT 780

Qy        782 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 841
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Db        781 GGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATA 840

Qy        842 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 901
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Db        841 CTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGA 900

Qy        902 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAG 961
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Db        901 ACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAG 960

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Qy       1022 GATCTATGATTTGGGCATCAAATATTCGT------------------------------ 1050
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Db       1021 GATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATA 1080

Qy       1051 ---------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1089
                                   ||||||||||||||||||||||||||||||||||||||
Db       1081 CGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGT 1140

Qy       1090 CTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGC 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGC 1200

Qy       1150 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1209
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Db       1201 TTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAA 1260

Qy       1210 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1269
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Db       1261 GTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAA 1320

Qy       1270 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAA 1329
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Db       1321 TAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAA 1379

Qy       1330 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1389
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Db       1380 AATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTC 1439

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Db       1440 AAGCAAGTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACG 1499

Qy       1450 CTGATCATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCT 1509
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Qy       1510 GCTCCAAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAAAAAAA 1569
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Qy       1570 AAA 1572
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Db       1620 ATA 1622
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RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

Query Match 87.2%; Score 1372; DB 9; Length 1728;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 5; Indels 163; Gaps 2;

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Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
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Db        123 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 182

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
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Db        183 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 242

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
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Db        243 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 302
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Qy       301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
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Db       303 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 362

Qy       361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
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Db       363 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 422

Qy       421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
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Db       423 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 482

Qy       481 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       483 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 542

Qy       541 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 600
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Db       543 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 602

Qy       601 TAGGCCAT---------------------------------------------------- 608
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Db       603 TAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTG 662

Qy       609 ------------------------------------------------------------A 609
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Db       663 TGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGA 722

Qy       610 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 669
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Db       723 ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACC 782

Qy       670 TGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 729
            |||||||  |||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       783 TGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCT 842

Qy       730 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 789
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       843 CGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTT 902

Qy       790 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 849
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       903 TCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGC 962

Qy       850 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 909
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       963 ATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTC 1022

Qy       910 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACAC 969
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      1023 TAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC 1082

Qy       970 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1029
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1083 ATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATG 1142

Qy      1030 ATTTGGGCATCAAATATTCGT---------------------------------------- 1050
            |||||||||||||||||||||
Db      1143 ATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCT 1202

Qy      1051 ------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1097
                        ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1203 TGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1262

Qy      1098 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1157
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1263 TAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTAT 1322

Qy      1158 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1217
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1323 TTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATC 1382

Qy      1218 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1277
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1383 CGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCT 1442

Qy      1278 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1337
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1443 ACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAA 1502

Qy      1338 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1397
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1503 AAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACT 1562

Qy      1398 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1457
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1563 TTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCAT 1622

Qy      1458 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1517
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1623 TGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAA 1682

Qy      1518 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAA 1563
            ||||||||||||||||||||||||||||||||||||||||||||||
Db      1683 TTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAAA 1728
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RESULT 4
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687

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;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (20)..(1304)
US-10-115-479-67

  Query Match            85.4%;  Score 1343.8;  DB 16;  Length 1743;
  Best Local Similarity  89.4%;  Pred. No. 0;
  Matches 1556;  Conservative    0;  Mismatches    7;  Indels  178;  Gaps    3;

Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 62

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         63 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 122

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 182

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 242

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 302

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 362

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 422

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 482

Qy        481 AGTACCCACTCTATGTTTTAA----------------AGGTTTCTGGAAAAGAACAAACAG 525
              |||||||||||||||||||||                |||||||||||||||||||| |||
Db        483 AGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAG 542

Qy        526 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 602

Qy        586 TCTGCTTGTGGTTCATAGGCCAT---------------------------------- 608
              |||||||||||||||||||||||
Db        603 TCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCA 662

Qy        609 ------------------------------------------------------------ 608

Db        663 ATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCAGTGGTTAATGTGGATGGTTATGACT 722

Qy        609 --------------AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 654
                             ||||||||||||||||||||||||||||||||||||||||||||
Db        723 ACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 782

Qy        655 GCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCAT 714
              |||||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||
Db        783 GCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCAT 842

Qy        715 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGA 902

Qy        775 AGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGC 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 AGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGC 962

Qy        835 ATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACC 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACC 1022

Qy        895 ATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAA 954
              |||||||||||||||||||||||||||||||||||||||||||||| |||| ||||||||
Db       1023 ATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAA 1082

Qy        955 ATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGG 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 ATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGG 1142

Qy       1015 ACGATTGGATCTATGATTTGGGCATCAAATATTCGT---------------------------- 1050
              |||||||||||||||||||||||||||||||||||
Db       1143 ACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGG 1202

Qy       1051 ----------------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTG 1082
                                          ||||||||||||||||||||||||||||||||
Db       1203 GCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTG 1262

Qy       1083 CCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATC 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 CCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATC 1322

Qy       1143 ATTCTGCTTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTA 1202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 ATTCTGCTTCCGTATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTA 1382

Qy       1203 TTTTTAAGTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAG 1262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 TTTTTAAGTTTTATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAG 1442

Qy       1263 AACCTAATAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT 1322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 AACCTAATAAGTGCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT 1502

Qy       1323 AAAAAAAAATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAG 1382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 AAAAAAAAATTGTAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAG 1562

Qy       1383 CCATCTCAAGCAACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCA 1442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 CCATCTCAAGCAACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCA 1622

Qy       1443 TCTCACGCTGATCATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAA 1502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 TCTCACGCTGATCATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAA 1682

Qy       1503 GATTTCTGCTCCAAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAA 1562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 GATTTCTGCTCCAAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAAAAAAAAA 1742

Qy       1563 A 1563
              |
Db       1743 A 1743


RESULT 5
US-10-115-479-69
; Sequence 69, Application US/10115479
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; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)..(1315)
US-10-115-479-69

  Query Match             59.3%;  Score 932.8;  DB 16;  Length 1344;
  Best Local Similarity   86.1%;  Pred. No. 3.6e-228;
  Matches 1145;  Conservative    0;  Mismatches    7;  Indels  178;  Gaps    3;

Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 73

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         74 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 133

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 193

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 253

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 313

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 373

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 433

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 493

Qy        481 AGTACCCACTCTATGTTTTAA--------------AGGTTTCTGGAAAAGAACAAACAG 525
              ||||||||||||||||||||              ||||||||||||||||||||| |||
Db        494 AGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAG 553

Qy        526 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 613

Qy        586 TCTGCTTGTGGTTCATAGGCCAT---------------------------------- 608
              |||||||||||||||||||||
Db        614 TCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCA 673

Qy        609 ------------------------------------------------------------ 608

Db        674 ATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACT 733

Qy        609 --------------AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 654
                            ||||||||||||||||||||||||||||||||||||||||||||||
Db        734 ACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 793

Qy        655 GCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCAT 714
              |||||||||||||||||||| |||||||  ||||||||||||||||||||||||||||||
Db        794 GCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCAT 853

Qy        715 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGA 913

Qy        775 AGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGC 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGC 973

Qy        835 ATTCATACTCCCAGCATATAGTGTTTCCTATTCCTATACACGAAGTAAAAGCAAAGACC 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATTCATACTCCCAGCATATAGTGTTTCCTATTCCTATACACGAAGTAAAAGCAAAGACC 1033

Qy        895 ATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAA 954
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||| ||||||||
Db       1034 ATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAA 1093

Qy        955 ATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGG 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 ATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGG 1153

Qy       1015 ACGATTGGATCTATGATTTGGGCATCAAATATTCGT----------------------- 1050
              |||||||||||||||||||||||||||||||||||
```

```
Db       1154 ACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGG 1213

Qy       1051 ----------------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTG 1082
                                            ||||||||||||||||||||||||||||||||
Db       1214 GCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTG 1273

Qy       1083 CCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATC 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 CCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATC 1333

Qy       1143 ATTCTGCTTC 1152
              ||||||||||
Db       1334 ATTCTGCTTC 1343


RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Papio hamadryas
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1269)
US-10-379-836-1

  Query Match           54.6%;  Score 858.8;  DB 15;  Length 1272;
  Best Local Similarity  83.9%;  Pred. No. 3.1e-209;
  Matches 1067;  Conservative    0;  Mismatches   42;  Indels  163;  Gaps    2;

Qy         18 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 77
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGCTTTGCAGTCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 60

Qy         78 TTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 137
              |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGCGTTTCAGAGTGGCCAGGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 120

Qy        138 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 197
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        121 GTGCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCGGAC 180

Qy        198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 257
              ||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 CTTATTGAGAAGAAAAAACAAGTCCATTTTTTTGTAAATTCATCTGATGTCGACAATGTG 240

Qy        258 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 317
              |||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||||
Db        241 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCCTGCTGGCAGATGTGGAAGAT 300

Qy        318 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 360

Qy        378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 437
              |||||||||||||||||||||||||||||||||||||||| |||||||||||| | ||||
Db        361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAACTTATAACTGAGAAGTAT 420

Qy        438 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 497
              |||||||||||||||||||||||||||||||| | ||||||| ||||||| ||||||

Db        421 CCTGATATGCTTACAAAAATCCACATTGGATCCTCCTATGAGAAGCACCCACTTTATGTT 480

Qy        498 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 557
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        481 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATGTGGATTGACTGTGGAATC 540

Qy        558 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT--------- 608
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCCAGAGAATGGATCTCCCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTGAA 600

Qy        609 ---------------------------------------------------------- 608

Db        601 TACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATG 660

Qy        609 -----------------------------------------AATCGAATGTGGAGAAAG 626
                                                        ||||||||||||||||||
Db        661 CCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 720

Qy        627 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGCAACTTTGTC 686
              ||||||||||||||||||||||||| |||||||||||||||||||| || |||||||
Db        721 AACCGTTCTTTCTATGCGAACAATCGTTGCATCGGAACAGACCTGAACAGGAACTTTGCG 780

Qy        687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        781 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGGAAACCTACTGTGGA 840

Qy        747 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 806
              |||||||||||||||||||||||| |||||| ||||||| ||||||||||||||||||||
Db        841 CTTTATCCTGAGTCAGAACCAGAAGCGAAGGCGGTGGCTAATTTCTTGAGAAGAAATATC 900

Qy        807 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 866
              |||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        901 AACCACATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATCGTGTTTCCATAT 960

Qy        867 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 926
              |||||||| ||||| |||||||||||||| |||||| |||||||||||||||||||||||
Db        961 TCCTATACTCGAAGCAAAAGCAAAGACCACGAGGAATTGTCTCTAGTAGCCAGTGAAGCA 1020

Qy        927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 986
              |||||||||||| | ||||| |||||||||| |||||||||||||||| ||||||||||
Db       1021 GTTCGTGCTATTCAGAAAACCAGTAAAAATATCAGGTATACACATGGCCGTGGCTCAGAA 1080

Qy        987 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1046
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       1081 ACCTTATACCTAGCTCCTGGAGGTGCGGACGATTGGATCTATGATTTGGGCATCAAATAT 1140

Qy       1047 TCGT----------------------------------------------------TTAC 1054
              ||||                                                    ||||
Db       1141 TCGTTTACAATTGAACTTCGAGATACGGGCAAATACGGATTCTTGCTGCCTGAGCGTTAC 1200

Qy       1055 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1114
              |||||||||| |||| ||| ||||||||||||||||||||||||||||||||||||||||
Db       1201 ATCAAACCCACTTGTAAAGACGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGTCATT 1260

Qy       1115 AGGAATGTTTAA 1126
              ||||||||||||
Db       1261 AGGAATGTTTAA 1272


RESULT 7
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
```

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;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

  Query Match          54.3%;  Score 853.8;  DB 9;  Length 1400;
  Best Local Similarity  93.3%;  Pred. No. 6.3e-208;
  Matches  934;  Conservative    1;  Mismatches   13;  Indels   53;  Gaps    2;

Qy       607 ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAG 666
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       177 AGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAG 236

Qy       667 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCAT 726
            |||||||||| |||||||  ||||||||||||||||||||||||||||||||||||||||
Db       237 ACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCAT 296

Qy       727 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTA 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       297 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTA 356

Qy       787 GTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCC 846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       357 GTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCC 416

Qy       847 AGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGT 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       417 AGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGT 476

Qy       907 CTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATA 966
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       477 CTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATA 536

Qy       967 CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCT 1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       537 CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCT 596

Qy      1027 ATGATTTGGGCATCAAATATTCGT---------------------------------- 1050
            |||||||||||||||||||||||
Db       597 ATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGAT 656

Qy      1051 ---------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTA 1094
                           ||||||||||||||||||||||||||||||||||||||||||||
Db       657 TCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTA 716

Qy      1095 AAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCG 1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       717 AAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCG 776

Qy      1155 TATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTT 1214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       777 TATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTT 836

Qy      1215 ATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGT 1274
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       837 ATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGT 896

Qy      1275 GCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTG 1334
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       897 GCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAAAATTG 955

Qy      1335 TAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA 1394
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       956 TAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA 1015

Qy      1395 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGAT 1454
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db      1016 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAWGATCATCTCACGCTGAT 1075

Qy      1455 CATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCC 1514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1076 CATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCC 1135

Qy      1515 AAATTTTCAATAAATTTCTTCTTCTCCTTAAAAAAAAAAA 1555
            |||||||||||||||||| ||| | | || | ||| | ||
Db      1136 AAATTTTCAATAAATTTCTGCTTGTGCCTTAGAAATACAA 1176


RESULT 8
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05913
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

  Query Match          54.3%;  Score 853.8;  DB 10;  Length 1400;
  Best Local Similarity  93.3%;  Pred. No. 6.3e-208;
  Matches  934;  Conservative    1;  Mismatches   13;  Indels   53;  Gaps    2;

Qy       607 ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAG 666
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       177 AGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAG 236

Qy       667 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCAT 726
            |||||||||| |||||||  ||||||||||||||||||||||||||||||||||||||||
Db       237 ACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCAT 296

Qy       727 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTA 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       297 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTA 356

Qy       787 GTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCC 846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       357 GTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCC 416

Qy       847 AGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGT 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       417 AGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGT 476

Qy       907 CTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATA 966
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       477 CTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATA 536

Qy       967 CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCT 1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       537 CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCT 596

Qy      1027 ATGATTTGGGCATCAAATATTCGT---------------------------------- 1050
            |||||||||||||||||||||||
Db       597 ATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGAT 656
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Qy       1051 ----------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTA 1094
                              ||||||||||||||||||||||||||||||||||||||||||||
Db        657 TCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTA 716

Qy       1095 AAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 AAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCG 776

Qy       1155 TATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTT 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 TATTTTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTT 836

Qy       1215 ATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 ATCCGTAGTTTTGATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGT 896

Qy       1275 GCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTG 1334
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        897 GCTACTTTGCCATTAAGGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAAAATTG 955

Qy       1335 TAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA 1394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 TAAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA 1015

Qy       1395 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGAT 1454
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db       1016 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAATCAAWGATCATCTCACGCTGAT 1075

Qy       1455 CATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCC 1514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 CATTGGATCCTACTCAACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCC 1135

Qy       1515 AAATTTTCAATAAATTTCTTCTTCTCCTTTAAAAAAAAAAA 1555
              |||||||||||||||||| ||| | | || | ||| | ||
Db       1136 AAATTTTCAATAAATTTCTGCTTGTGCCTTTAGAAATACAA 1176
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RESULT 9
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63

Query Match 43.7%; Score 688; DB 16; Length 1037;
Best Local Similarity 79.3%; Pred. No. 1.6e-165;
Matches 955; Conservative 0; Mismatches 5; Indels 244; Gaps 2;

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Qy          1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 83

Qy         61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         84 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 143

Qy        121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 203

Qy        181 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCAT 263

Qy        241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 323

Qy        301 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAG 383

Qy        361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 443

Qy        421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        444 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTGAGA 503

Qy        481 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATAT 540
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        504 AGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATAT 563

Qy        541 GGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCA 600
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          ||||||
Db       564 GGATTG---------------------------------------------------------- 569

Qy       601 TAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCG 660

Db       570 ---------------------------------------------------------- 569

Qy       661 GAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTT 720

Db       570 ---------------------------------------------------------- 569

Qy       721 CCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAG 780
                         ||||||||||||||||||||||||||||||||||||||||||||||
Db       570 ------------------ACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAG 611

Qy       781 TGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCAT 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       612 TGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCAT 671

Qy       841 ACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       672 ACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGG 731

Qy       901 AACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACTAGTAAAAATACCA 960
             |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db       732 AACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCA 791

Qy       961 GGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       792 GGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATT 851

Qy       1021 GGATCTATGATTTGGGCATCAAATATTCGT---------------------------- 1050
              ||||||||||||||||||||||||||||
Db        852 GGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACAT 911

Qy       1051 ----------------------TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTG 1088
                                    ||||||||||||||||||||||||||||||||||||
Db        912 ACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTG 971

Qy       1089 TCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTG 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 TCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTG 1031

Qy       1149 CTTC 1152
              ||||
Db       1032 CTTC 1035
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RESULT 10
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
;   LENGTH: 1132
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1103)
US-10-115-479-65

  Query Match           38.8%;  Score 610.4;  DB 16;  Length 1132;
  Best Local Similarity  85.2%;  Pred. No. 1.3e-145;
  Matches  760;  Conservative    0;  Mismatches    6;  Indels  126;  Gaps    2;
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Qy         1 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        24 AGAAAATTGCTGTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCT 83

Qy        61 TCTGTGAGCAGCATGTCTTCGCGTTCCACAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 120
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        84 TCTGTGAGCAGCATGTCTTCGCGTTTCACAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAA 143

Qy       121 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       144 CCTCTAGGCAAGTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGC 203

Qy       181 AGCCGGTAACAGCTGACCTTATTGTGAACAAAAAACAAGTCCATTTTTTTGTAAATGCAT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       204 AGCCGGTAACAGCTGACCTTATTGTGAACAAAAAACAAGTCCATTTTTTTGTAAATGCAT 263

Qy       241 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       264 CTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGC 323

Qy       301 TGGCAGACGTGGAAGATCTTATTCAACACCAGATTTCCAACGACACAGTCAGCCCCCGAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       324 TGGCAGACGTGGAAGATCTTATTCAACACCAGATTTCCAACGACACAGTCAGCCCCCGAG 383

Qy       361 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       384 CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT 443
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Qy       421 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       444 TTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGA 503

Qy       481 AGTACCCACTCTATGTTTTAA----------------AGGTTTCTGGAAAAGAACAAACAG 525
            |||||||||||||||||||||                ||||||||||||||||||| |||
Db       504 AGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAG 563

Qy       526 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 585
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       564 CCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTT 623

Qy       586 TCTGCTTGTGGTTCATAGGCCAT---------------------------------- 608
            |||||||||||||||||||||||
Db       624 TCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCA 683

Qy       609 ---------------------------------------------------------- 608

Db       684 ATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACT 743

Qy       609 --------------AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 654
                           ||||||||||||||||||||||||||||||||||||||||||||||
Db       744 ACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATT 803

Qy       655 GCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCAT 714
            |||||||||||||||||||||| |||||||  ||||||||||||||||||||||||||||||
Db       804 GCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCAT 863

Qy       715 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACC 766
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       864 CCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAAAC 915
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RESULT 11
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 30.4%; Score 478.6; DB 9; Length 55827;
Best Local Similarity 98.0%; Pred. No. 5.8e-111;
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Qy      1051 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 1110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53334 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 53393

Qy      1111 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 1170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53394 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 53453

Qy      1171 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 1230
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53454 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 53513

Qy      1231 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 1290
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53514 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 53573

Qy      1291 GGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAAAAGTCTAGTTACC 1350
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     53574 GGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAAAATTGTAAAAGTCTAGTTACC 53632

Qy      1351 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 1410
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53633 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 53692

Qy      1411 TAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCATTGGATCCTACTCA 1470
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     53693 TAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACGCTGATCATTGGATCCTACTCA 53752

Qy      1471 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 1530
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53753 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 53812

Qy      1531 TCTTCTTCTCCTTTAAAAAAAAAAA 1555
            ||| ||| | | || | ||| | ||
Db     53813 TCTGCTTGTGCCTTTAGAAATACAA 53837
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RESULT 12
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Query Match 30.4%; Score 478.6; DB 14; Length 55827;
Best Local Similarity 98.0%; Pred. No. 5.8e-111;
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

```
Qy      1051 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 1110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53334 TTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAATAGCTTGGCATGT 53393

Qy      1111 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 1170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53394 CATTAGGAATGTTTAATGCCCCTGATTTTATCATTCTGCTTCCGTATTTTAATTTACTGA 53453

Qy      1171 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 1230
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53454 TTCCAGCAAGACCAAATCATTGTATCAGATTATTTTTAAGTTTTATCCGTAGTTTTGATA 53513

Qy      1231 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 1290
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53514 AAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAA 53573

Qy      1291 GGCAGACTAGGGTTCATGTCTTTTTACCCTTTAAAAAAAAATTGTAAAAGTCTAGTTACC 1350
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     53574 GGCAGACTAGGGTTCATGTCTTTTTACCCTTT-AAAAAAAATTGTAAAAGTCTAGTTACC 53632

Qy      1351 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 1410
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53633 TACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAACTTTCGACGTTTGAC 53692

Qy      1411 TAGCCATCTCAAGCAAGTTTAATCAAAGATCATCTCACGCTGATCATTGGATCCTACTCA 1470
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            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      53693 TAGCCATCTCAAGCAAGTTTAATCAATGATCATCTCACGCTGATCATTGGATCCTACTCA 53752

Qy       1471 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 1530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53753 ACAAAAGGAAGGGTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATT 53812

Qy       1531 TCTTCTTCTCCTTTAAAAAAAAAAA 1555
              ||| ||| | | || | ||| | ||
Db      53813 TCTGCTTGTGCCTTTAGAAATACAA 53837


RESULT 13
US-09-960-352-14595
; Sequence 14595, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14595
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 62-LIB34-032-Q1-E1-H10
US-09-960-352-14595

  Query Match             21.1%;  Score 331.2;  DB 9;  Length 416;
  Best Local Similarity   87.3%;  Pred. No. 2.5e-74;
  Matches  363;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy        167 GATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTT 226
              |||||||||||||||||| ||| |||||||   |||||||||  | |  ||||||||||
Db          1 GATTGTTCTCTGGCAGCCAGTAGCAGCTGAATATATTGTGAAGGGATACGAAGTCCATTT 60

Qy        227 TTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCCCATTTAAATGTGAGCGGAATTCC 286
              ||||||  ||||||||||||||   |||||||||||||||||||||| |||| |||||||
Db         61 TTTTGTGAATGCATCTGATGTAAGCAATGTGAAAGCCCATTTAAATGCGAGCAGAATTCC 120

Qy        287 ATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACAC 346
              || ||| ||| || ||| | | |||||||||||||| |  ||||||| |||||| |||||
Db        121 ATTCAGGGTCCTGGTGGAAAATGTGGAAGATCTTATCCGGCAGCAGACTTCCAATGACAC 180

Qy        347 AGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTA 406
               ||||||||||  || ||| | || |||||||||||||||||||||||||||| |||||
Db        181 CATCAGCCCCCGGGCATCCTCCTCCTACTATGAACAGTATCACTCACTAAATGAGATCTA 240

Qy        407 TTCTTGGATAGAATTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGG 466
              |||||||||||| |||| |||||| || |||||||||| ||  ||||||||||||||
Db        241 TTCTTGGATAGAAGTTATGACTGAGCGGTATCCTGATATGGTTGAAAAAATCCACATTGG 300

Qy        467 ATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGC 526
              ||||||||  |||||||||||||| ||||||||||||||||  ||||||||||   ||
Db        301 ATCCTCATACGAGAAGTACCCACTTTATGTTTTAAAGGTTTCTAAAAAAGAACAAAGGGC 360

Qy        527 CAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTG 582
              |||||||||||| |||||||||||||||||| |||||||| ||||||||||||
Db        361 CAAAAATGCCATGTGGATTGACTGTGGAATCCACGCCAGAGAGTGGATCTCTCCTG 416


RESULT 14
US-09-960-352-8425
; Sequence 8425, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8425
;   LENGTH: 397
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 36-LIB34-005-Q1-E1-A12
US-09-960-352-8425

  Query Match             18.2%;  Score 286.8;  DB 9;  Length 397;
  Best Local Similarity   83.9%;  Pred. No. 5.8e-63;
  Matches  324;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy         12 GTTGGGATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAG 71
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Db         12 GTGGGGATGAAGCTTTATAGCTTGGGAGTCCTTGTCGCCACCGTCCTGTTCTGTGGGGAG 71

Qy         72 CATGTCTTCGCGTTCCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAA 131
              |||| |||||| || ||||| ||||| ||| || ||||||||||||||||||| ||||||
Db         72 CATGCCTTCGCCTTTCAGAGGGGCCAGGTTTTATCTGCTCTTCCTAGAACCTCCAGGCAA 131

Qy        132 GTTCAAGTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACA 191
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Db        132 GTTCAAATTCTGCAGAATGTTACTACAACATACAAGATTGTTCTCTGGCAGCCAGTAGCA 191

Qy        192 GCTGACCTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGAC 251
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Db        192 GCTGAATATATTGTGAAGGGATACGAAGTCCATTTTTTTGTGAATGCATCTGATGTAAGC 251

Qy        252 AATGTGAAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTG 311
              |||||||||||||||||||||| |||| |||||||||| ||| ||| || ||| | | |||
Db        252 AATGTGAAAGCCCATTTAAATGCGAGCAGAATTCCATTCAGGGTCCTGGTGGAAAATGTG 311

Qy        312 GAAGATCTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCG 371
              |||||||||| |  ||||||| |||||| |||||  |||||||||| || ||| | ||
Db        312 GAAGATCTTATCCGGCAGCAGACTTCCAATGACACCATCAGCCCCCGGGCATCCTCCTCC 371

Qy        372 TACTATGAACAGTATCACTCACTAAA 397
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Db        372 TACTATGAACAGTATCACTCACTAAA 397


RESULT 15
US-09-917-800A-468/c
; Sequence 468, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5038-US
;  CURRENT APPLICATION NUMBER: US/09/917,800A
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
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;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 1740
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA998857
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(431)
;   OTHER INFORMATION: n = a or c or g or t
US-09-917-800A-468

  Query Match             8.7%;  Score 137.2;  DB 9;  Length 431;
  Best Local Similarity   67.5%;  Pred. No. 1.3e-24;
  Matches  268;  Conservative    0;  Mismatches   69;  Indels   60;  Gaps    3;

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Db        431 CATGAGGAACTGTCTNTAGTGGCCAGCGAAGCAGTTCGTGCCATTGAAAGTATTAATAAA 372

Qy        954 AATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGG 1013
              || |||||||| |||||||||  |||||||||||  ||||| ||||||||||||||||
Db        371 AACACCAGGTACACACATGGCAGTGGCTCAGAAAGTTTATATCTAGCTCCTGGAGGTTCT 312

Qy       1014 GACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTA---------------------- 1053
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Db        311 GATGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACGATTGAACTTCGGGATACA 252

Qy       1054 --------------------------------CATCAAACCCACCTGTAGAGAAGCTTTT 1081
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Db        251 GGCAGATACGGGTTCTTGCTGCCTGAGAGATTCATCAAACCCACTTGCGCAGAAGCTTTG 192

Qy       1082 GCCGCTGTCTCTAAAATAGCTTGGCATGTCATTAGGAATGTTTAATGCCCCTGATTTTAT 1141
              |||||| |||||||||||||||||||||||| |||||   ||||  |||       ||
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              |  |   ||       ||||| |||| ||||| |||||| || ||||  ||| |  || |
Db        137 CTCTGCTCTCATTACTTTTATTTTATTGATTTCAGCAACACTAAATTGTTGCACTAGCTT 78

Qy       1201 -TATTTTTAAGTTTTATCCGTAGTTTTGATAAAAGAT 1236
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Db         77 CTAAGTTTAATCAGTTTCCTTGGTTTTGTTGAAGAAT 41


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Job time : 821 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 19:34:50 ; Search time 27.4576 Seconds
(without alignments)
869.503 Million cell updates/sec

Title: US-09-980-881A-2
Perfect score: 1911
Sequence: 1 MKLCSLAVLVPIVLFCEQHV.....IKYSFTSNPPVEKLLPLSLK 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1817	95.1	386	4	US-09-813-133A-2	Sequence 2, Appli
2	1799.5	94.2	423	1	US-07-649-591B-3	Sequence 3, Appli
3	1799.5	94.2	423	1	US-08-277-540-3	Sequence 3, Appli
4	1799.5	94.2	423	1	US-08-430-787A-3	Sequence 3, Appli
5	1799.5	94.2	423	2	US-08-869-057-2	Sequence 2, Appli
6	1788.5	93.6	423	4	US-09-813-133A-4	Sequence 4, Appli
7	640.5	33.5	404	1	US-08-696-139-2	Sequence 2, Appli
8	639	33.4	415	2	US-08-860-882A-57	Sequence 57, Appl
9	639	33.4	415	4	US-09-011-769A-39	Sequence 39, Appl
10	631.5	33.0	424	4	US-09-011-769A-56	Sequence 56, Appl
11	628.5	32.9	417	1	US-07-649-591B-7	Sequence 7, Appli
12	628.5	32.9	417	1	US-08-277-540-7	Sequence 7, Appli
13	628.5	32.9	417	1	US-08-430-787A-7	Sequence 7, Appli
14	623	32.6	716	3	US-09-171-945-125	Sequence 125, App
15	619.5	32.4	417	1	US-07-649-591B-6	Sequence 6, Appli
16	619.5	32.4	417	1	US-08-277-540-6	Sequence 6, Appli
17	619.5	32.4	417	1	US-08-430-787A-6	Sequence 6, Appli
18	619.5	32.4	417	4	US-09-917-254-66	Sequence 66, Appl
19	604	31.6	307	2	US-08-782-760-6	Sequence 6, Appli
20	604	31.6	307	5	PCT-US96-00995-6	Sequence 6, Appli
21	604	31.6	437	4	US-09-675-305-10	Sequence 10, Appl
22	604	31.6	437	4	US-10-200-344-10	Sequence 10, Appl
23	603.5	31.6	396	1	US-07-649-591B-4	Sequence 4, Appli
24	603.5	31.6	396	1	US-08-277-540-4	Sequence 4, Appli
25	603.5	31.6	396	1	US-08-430-787A-4	Sequence 4, Appli
26	576	30.1	306	1	US-08-696-139-4	Sequence 4, Appli
27	561	29.4	329	4	US-09-011-769A-51	Sequence 51, Appl
28	561	29.4	349	4	US-09-011-769A-47	Sequence 47, Appl
29	554	29.0	349	4	US-09-011-769A-60	Sequence 60, Appl
30	553	28.9	349	4	US-09-011-769A-64	Sequence 64, Appl
31	553	28.9	417	1	US-07-649-591B-8	Sequence 8, Appli
32	553	28.9	417	1	US-08-277-540-8	Sequence 8, Appli
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34	546	28.6	399	4	US-09-710-099-8	Sequence 8, Appli
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36	543	28.4	613	3	US-09-171-945-113	Sequence 113, App
37	528.5	27.7	350	4	US-09-675-305-12	Sequence 12, Appl
38	528.5	27.7	350	4	US-10-200-344-12	Sequence 12, Appl
39	528.5	27.7	419	1	US-07-649-591B-5	Sequence 5, Appli
40	528.5	27.7	419	1	US-08-277-540-5	Sequence 5, Appli
41	528.5	27.7	419	1	US-08-430-787A-5	Sequence 5, Appli
42	519.5	27.2	436	4	US-09-710-099-6	Sequence 6, Appli
43	519.5	27.2	436	4	US-10-200-910-6	Sequence 6, Appli
44	513	26.8	417	3	US-08-640-906-4	Sequence 4, Appli
45	513	26.8	417	3	US-09-395-936-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 95.1%; Score 1817; DB 4; Length 386;
Best Local Similarity 98.6%; Pred. No. 4.9e-189;
Matches 341; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
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Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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Db        301 SEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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RESULT 2

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US-07-649-591B-3
; Sequence 3, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-3

  Query Match             94.2%;  Score 1799.5;  DB 1;  Length 423;
  Best Local Similarity   89.6%;  Pred. No. 4.6e-187;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
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Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
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Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
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Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||||||||||||||||||
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RESULT 3
US-08-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-3

  Query Match             94.2%;  Score 1799.5;  DB 1;  Length 423;
  Best Local Similarity   89.6%;  Pred. No. 4.6e-187;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||                                   ||||||
Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
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Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300
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Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
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Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
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Db        361 TLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 4
US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-3

  Query Match             94.2%;  Score 1799.5;  DB 1;  Length 423;
  Best Local Similarity   89.6%;  Pred. No. 4.6e-187;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHPFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHPFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH----------------------------------NRMWRK 203
              |||||||||||||||||                                  ||||||
Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
              |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||||||||||||||||||
Db        361 TLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 5
US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Plasma
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23..401
US-08-869-057-2

  Query Match             94.2%;  Score 1799.5;  DB 2;  Length 423;
  Best Local Similarity   89.6%;  Pred. No. 4.6e-187;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
               |||||||||||||||||                                   ||||||
Db         181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy         204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
               ||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db         241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy         264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
               ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360

Qy         324 TLYLAPGGGDDWIYDLGIKYSFT 346
               |||||||||||||||||||||||
Db         361 TLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 6
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

  Query Match            93.6%;  Score 1788.5;  DB 4;  Length 423;
  Best Local Similarity  89.0%;  Pred. No. 7.2e-186;
  Matches  341;  Conservative    1;  Mismatches    4;  Indels   37;  Gaps    1;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180
               |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
               |||||||||||||||||                                   ||||||
Db         181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy         204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
               |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db         241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy         264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
               ||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||||||
Db         301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSE 360

Qy         324 TLYLAPGGGDDWIYDLGIKYSFT 346
               |||||||||||||||||||||||
Db         361 TLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 7
US-08-696-139-2
; Sequence 2, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  404 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-696-139-2

  Query Match            33.5%;  Score 640.5;  DB 1;  Length 404;
  Best Local Similarity  37.7%;  Pred. No. 7.8e-61;
  Matches  136;  Conservative   60;  Mismatches  122;  Indels   43;  Gaps    6;

Qy          23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82
               |:  :|          : :|  | :| :|  |:| :   |      | | | | |:  |:
Db          10 FEGEKVFRVNVEDENDISLLHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVED 69

Qy          83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142
                 |  : :   ||: ::  ::: |  :     | :   ||:|::   | :| : :|  :||
Db          70 FLEQNELQYEVLINNLRSVLEAQFDSRV---RTTGHSYEKYNNWETIEAWTKQVTSENPD 126

Qy         143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 195
               ::::  ||::|    :|:||| ||     | ||::||| ||||||| ||| ||:
Db         127 LISRTAIGTTFLGNNIYLLKV-GKPGPNKPAIFMDCGFHAREWISHAFCQWFVREAVLTY 185

Qy         196 ----------------------GH------NRMWRKNRSFYANNHCIGTDLNSNFVSK 225
                                    |:      |||||| ||  |   ||||| | ||
Db         186 GYESHMTEFLNKLDFYVLPVLNIDGYIYTWTKNRMWRKTRSTNAGTTCIGTDPNRNF-DA 244
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Qy        226 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 285
              ||  |||:  | |||||   ||| | ||:| |:| |:: ||||:::|||||  |::|||| 
Db        245 GWCTTGASTDPCDETYCGSAAESEKETKALADFIRNNLSSIKAYLTIHSYSQMILYPYSY 304

Qy        286 TRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 345
                  ::: ||: :|  ||: :  |   |:||:| |: |:| | || ||| || ||||||  
Db        305 DYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGATTIYPAAGGSDDWAYDQGIKYSF 363

Qy        346 T 346
              |
Db        364 T 364
```

```
RESULT 8
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  415 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-860-882A-57

  Query Match            33.4%;  Score 639;  DB 2;  Length 415;
  Best Local Similarity   35.6%;  Pred. No. 1.2e-60;
  Matches  135;  Conservative   69;  Mismatches  131;  Indels   44;  Gaps    7;

Qy          6 LAVLVPIVLFCEQHVFA-FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVK 64
              | ||| : |     |    |:  :|         : ::: | :| :|  |:| :   |
Db          2 LLVLVTVALASAHHGGEHFEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKP 61

Qy         65 KKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYH 124
                  | | | | |   |:  |  : :   ||:::: :::: |  :     ||:   ||:|:
Db         62 HSTVDFRVKAEDTVTVENVLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYN 118

Qy        125 SLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHARE 184
                 | :| : :   :| ::::  ||::||   :|:||| ||    | ||::||| ||||
Db        119 KWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHARE 177

Qy        185 WISPAFCLWFI----------------------------------GH------NRMWRKNRSF 207
              ||||||| ||:                                  |:      :| ||| ||
Db        178 WISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRST 237

Qy        208 YANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIK 267
              :  : ||||| | ||    ||| ||| : | |||||   ||| | ||:| |:|  :: ||
Db        238 HTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIK 296

Qy        268 AYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
              ||:::||||| :::|||||     ::: ||: :|   |: :  :   |:||:| |: |:| 
Db        297 AYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYP 355

Qy        328 APGGGDDWIYDLGIKYSFT 346
              | || ||| || ||:|||| 
Db        356 AAGGSDDWAYDQGIRYSFT 374
```

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RESULT 9
US-09-011-769A-39
; Sequence 39, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 39:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 415 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39

  Query Match            33.4%;  Score 639;  DB 4;  Length 415;
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  Best Local Similarity   35.6%;  Pred. No. 1.2e-60;
  Matches  135;  Conservative   69;  Mismatches  131;  Indels   44;  Gaps    7;

Qy          6 LAVLVPIVLFCEQHVFA-FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVK 64
              | ||| : |     |    |:  :|          : ::: | :| :|  :|:| :    |
Db          2 LLVLVTVALASAHHGGEHFEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKP 61

Qy         65 KKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYH 124
                | | | | |    |:  |  : :   ||:::: :::: |  :     ||:   ||:|:|
Db         62 HSTVDFRVKAEDTVTVENVLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYN 118

Qy        125 SLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHARE 184
                | :| : :   :| ::::  ||::||   :|:||| ||    | ||::||| ||||
Db        119 KWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHARE 177

Qy        185 WISPAFCLWFI------------------------------GH------NRMWRKNRSF 207
              ||||||| ||:                            |:      :| ||| ||
Db        178 WISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRST 237

Qy        208 YANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIK 267
              :  : ||||| | ||    ||| ||| : | |||||   ||| | ||:| |:|  :: ||
Db        238 HTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIK 296

Qy        268 AYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
              ||:::|||| :::|||     ::: ||: :|   |: :  :   |:||:| |: |:|
Db        297 AYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYP 355

Qy        328 APGGGDDWIYDLGIKYSFT 346
              | || ||| || ||:||||
Db        356 AAGGSDDWAYDQGIRYSFT 374


RESULT 10
US-09-011-769A-56
; Sequence 56, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;  INFORMATION FOR SEQ ID NO: 56:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 424 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-011-769A-56

  Query Match             33.0%;  Score 631.5;  DB 4;  Length 424;
  Best Local Similarity   35.7%;  Pred. No. 8.1e-60;
  Matches  129;  Conservative   68;  Mismatches  121;  Indels   43;  Gaps    6;

Qy         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82
              |:  :|          : ::: | :| :|  :|: :    |      | | | | |   |:
Db         29 FEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKPHSTVDFRVKAEDTVTVEN 88

Qy         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142
               |  : :   ||:::: :::: |  :     ||:   ||:|:    | :| : :   :|
Db         89 VLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYNKWETIEAWTQQVATENPA 145

Qy        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 195
              ::::  ||::||   :|:||| ||    | ||::||| |||||||||| ||:
Db        146 LISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHAREWISPAFCQWFVREAVRTY 204

Qy        196 ------------------------GH------NRMWRKNRSFYANNHCIGTDLNSNFVSK 225
                                     |:      :| ||| || :  : |||| | ||
Db        205 GREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRSTHTGSSCIGTDPNRNF-DA 263

Qy        226 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 285
              ||| ||| : | |||||   ||| | ||:| |:|  :: ||||:::||||| :::||||
Db        264 GWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIKAYLTIHSYSQMMIYPYSY 323

Qy        286 TRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 345
                  ::: ||: :|   |: :  :   |:||:| |: |:| | || ||| || ||:|||
Db        324 AYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYPAAGGSDDWAYDQGIRYSF 382

Qy        346 T 346
              |
Db        383 T 383


RESULT 11
US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
```

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;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-7

  Query Match            32.9%;  Score 628.5;  DB 1;  Length 417;
  Best Local Similarity  37.0%;  Pred. No. 1.7e-59;
  Matches  140;  Conservative   60;  Mismatches  131;  Indels   47;  Gaps    8;

Qy          6 LAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKK 65
              :||:   :      |   |   :|     :  :   ||:||| : |:  | |     |
Db          7 MAVIYTTLAIAPVH---FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVN 63

Qy         66 KQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYH 124
               | | |:  :   ::: |   |   :|: |::: |::|    | :: | |   | :|:
Db         64 MTVDFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYN 120

Qy        125 SLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHARE 184
              ::| || | : |:||:|:::| |||: |  ||||||: ||:   : ||::|||||||||
Db        121 DWDKIVSWTEKMLEKHPEMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHARE 179

Qy        185 WISPAFCLWFI-------GHN-----------------------------RMWRKNRSF 207
              ||||||| ||:       | |                             ||||||||
Db        180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFYVLPVFNVDGYIWSWTQDRMWRKNRSR 239

Qy        208 YANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIK 267
              |: ||||||| ||     |      ::   |   | |  |||| | ||| :|:| ::| ||
Db        240 NQNSTCIGTDLNRNF-DVSWDSSPNTNKPCLNVYRGPAPESEKETKAVTNFIRSHLNSIK 298

Qy        268 AYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
              |||: |||||  :: || ||      :|::|  ||  |  |:  |   ||| :|  : |:|
Db        299 AYITFHSYSQMLLIPYGYTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYK 357

Qy        328 APGGGDDWIYDLGIKYSF 345
              |   ||:||||||::|
Db        358 TSGSSLDWVYDLGIKHTF 375


RESULT 12
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-7

  Query Match            32.9%;  Score 628.5;  DB 1;  Length 417;
  Best Local Similarity  37.0%;  Pred. No. 1.7e-59;
  Matches  140;  Conservative   60;  Mismatches  131;  Indels   47;  Gaps    8;

Qy          6 LAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKK 65
              :||:   :      |   |   :|     :  :   ||:||| : |:  | |     |
Db          7 MAVIYTTLAIAPVH---FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVN 63

Qy         66 KQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYH 124
               | | |:  :   ::: |   |   :|: |::: |::|    | :: | |   | :|:
Db         64 MTVDFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYN 120

Qy        125 SLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHARE 184
              ::| || | : |:||:|:::| |||: |  ||||||: ||:   : ||::|||||||||
Db        121 DWDKIVSWTEKMLEKHPEMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHARE 179

Qy        185 WISPAFCLWFI-------GHN-----------------------------RMWRKNRSF 207
              ||||||| ||:       | |                             ||||||||
Db        180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFYVLPVFNVDGYIWSWTQDRMWRKNRSR 239

Qy        208 YANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIK 267
              |: ||||||| ||     |      ::   |   | |  |||| | ||| :|:| ::| ||
Db        240 NQNSTCIGTDLNRNF-DVSWDSSPNTNKPCLNVYRGPAPESEKETKAVTNFIRSHLNSIK 298

Qy        268 AYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
              |||: |||||  :: || ||      :|::|  ||  |  |:  |   ||| :|  : |:|
Db        299 AYITFHSYSQMLLIPYGYTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYK 357

Qy        328 APGGGDDWIYDLGIKYSF 345
              |   ||:||||||::|
Db        358 TSGSSLDWVYDLGIKHTF 375


RESULT 13
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-7

  Query Match             32.9%;  Score 628.5;  DB 1;  Length 417;
  Best Local Similarity   37.0%;  Pred. No. 1.7e-59;
  Matches  140;  Conservative   60;  Mismatches  131;  Indels   47;  Gaps    8;

Qy          6 LAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKK 65
              :||:   :      |   |   :|     :  :   ||:||| : |:  | |     |
Db          7 MAVIYTTLAIAPVH---FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVN 63

Qy         66 KQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYH 124
                | | |:  :   ::: |     |   :|: |::: |::|     | :: | |   | :|:
Db         64 MTVDFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYN 120

Qy        125 SLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHARE 184
              ::| || | : |:||:|:::| |||: |  ||||||: ||:   : ||::|||||||||
Db        121 DWDKIVSWTEKMLEKHPEMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHARE 179

Qy        185 WISPAFCLWFI-------GHN-----------------------------RMWRKNRSF 207
              ||||||| ||:       | |                             ||||||||
Db        180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFYVLPVFNVDGYIWSWTQDRMWRKNRSR 239

Qy        208 YANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIK 267
                |: ||||||| ||     |      ::  |   | |  |||| | ||| :|:| ::| ||
Db        240 NQNSTCIGTDLNRNF-DVSWDSSPNTNKPCLNVYRGPAPESEKETKAVTNFIRSHLNSIK 298

Qy        268 AYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
              |||: |||||  ::  || ||     :|::|  ||  |  |:  |   ||| :|  : |:|
Db        299 AYITFHSYSQMLLIPYGYTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYK 357

Qy        328 APGGGDDWIYDLGIKYSF 345
                |   ||:||||||::|
Db        358 TSGSSLDWVYDLGIKHTF 375


RESULT 14
US-09-171-945-125
; Sequence 125, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;  APPLICANT:  Emery, Stephen
;  APPLICANT:  Copley, Clive Graham
;  APPLICANT:  Edge, Michael Derek
;  TITLE OF INVENTION:  Monoclonal Antibody to CEA, Conjugates Comprising Said
;  TITLE OF INVENTION:  Antibody, and Their Therapeutic Use in an Adept System
;  FILE REFERENCE:  Monoclonal Antibody to CEA
;  CURRENT APPLICATION NUMBER: US/09/171,945
;  CURRENT FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  GB9703103.3
;  PRIOR FILING DATE:  1997-02-14
;  PRIOR APPLICATION NUMBER:  GB9609405.7
;  PRIOR FILING DATE:  1996-05-04
;  PRIOR APPLICATION NUMBER:  PCT/GB97/01165
;  PRIOR FILING DATE:  1997-04-29
;  NUMBER OF SEQ ID NOS:  131
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 125
;  LENGTH: 716
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-125

  Query Match             32.6%;  Score 623;  DB 3;  Length 716;
  Best Local Similarity   34.6%;  Pred. No. 1.6e-58;
  Matches  132;  Conservative   72;  Mismatches  134;  Indels   44;  Gaps    7;

Qy          3 LCSLAVLVPIVLFCEQHVFA-FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADL 61
              : :| ||| : |     |    |:  :|          : ::: | :| :|  |:| :
Db          1 MLALLVLVTVALASAHHGGEHFEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQ 60

Qy         62 IVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYE 121
              |     | | | | |    |:  |  : :   ||:::: :::: |  :     ||:   ||
Db         61 IKPHSTVDFRVKAEDTVTVENVLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYE 117

Qy        122 QYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIH 181
              :|:    | :| : :   :| :::: ||::||   :|:||| ||    | ||::||| |
Db        118 KYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFH 176

Qy        182 AREWISPAFCLWFI----------------------------GH------NRMWRKN 204
              |||||||||| ||:                            |:      :| |||
Db        177 AREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKT 236

Qy        205 RSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNIN 264
              || :  : ||||| | ||    ||| ||| : | |||||   ||| | ||:| |:|  ::
Db        237 RSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLS 295

Qy        265 QIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSET 324
              ||||:::||||| :::|||| :::  ||: :|  |: :  :  |:||:| |: |
Db        296 SIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATT 354

Qy        325 LYLAPGGGDDWIYDLGIKYSFT 346
              :| : |  || || ||:||||
Db        355 IYPSAGTSKDWAYDQGIRYSFT 376


RESULT 15
US-07-649-591B-6
; Sequence 6, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Baton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-6

  Query Match            32.4%;  Score 619.5;  DB 1;  Length 417;
  Best Local Similarity  34.1%;  Pred. No. 1.6e-58;
  Matches  130;  Conservative   76;  Mismatches  128;  Indels   47;  Gaps    8;

Qy          6 LAVLVPIVLFCEQHVFA---FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLI 62
              : :::|: |        |   |   :|    |:  :|  ::::|  | |:  | |     :
Db          1 MRLILPVGLIATTLAIAPVRFDREKVFRVKPQDEKQADIIKDLAKTNELDFWYPGATHHV 60

Qy         63 VKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYE 121
                | | |:  :   ::: |: : :   :|: |::: |::|    : :  | |   |
Db         61 AANMMVDFRVSEKESQAIQSALDQNKMHYEILIHDLQEEIEKQFDVKEDIPGRHS---YA 117

Qy        122 QYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIH 181
              :|::  :| :| | : :::|:|:::| |||: |  ||||||: |::   : ||::|||||
Db        118 KYNNWEKIVAWTEKMMDKYPEMVSRIKIGSTVEDNPLYVLKI-GEKNERRKAIFMDCGIH 176

Qy        182 AREWISPAFCLWFI------------------------------GH------NRMWRKN 204
              ||||:|||||  ||:                              |:      |||||||
Db        177 AREWVSPAFCQWFVYQATKTYGRNKIMTKLLDRMNFYILPVFNVDGYIWSWTKNRMWRKN 236

Qy        205 RSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNIN 264
              ||   |: ||||||| || :  |     ::  |:: | |  |||| | ||| :|:| ::|
Db        237 RSKNQNSKCIGTDLNRNF-NASWNSIPNTNDPCADNYRGSAPESEKETKAVTNFIRSHLN 295

Qy        265 QIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSET 324
              :|| ||: ||||| ::||| ||     :||:|: ||      :  |   ||| :|    |
Db        296 EIKVYITFHSYSQMLLFPYGYTSKLPPNHEDLAKVAKIGTDVL-STRYETRYIYGPIEST 354

Qy        325 LYLAPGGGDDWIYDLGIKYSF 345
              :|   |   || ||||||::|
Db        355 IYPISGSSLDWAYDLGIKHTF 375


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Job time : 29.4576 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:43:44 ; Search time 82.3729 Seconds
(without alignments)
1416.943 Million cell updates/sec

Title: US-09-980-881A-2
Perfect score: 1911
Sequence: 1 MKLCSLAVLVPIVLFCEQHV.....IKYSFTSNPPVEKLLPLSLK 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1817	95.1	386	9	US-09-813-133A-2	Sequence 2, Appli
2	1817	95.1	386	14	US-10-212-877-2	Sequence 2, Appli
3	1799.5	94.2	423	14	US-10-379-836-17	Sequence 17, Appl
4	1788.5	93.6	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1788.5	93.6	423	14	US-10-212-877-4	Sequence 4, Appli
6	1776	92.9	428	15	US-10-115-479-68	Sequence 68, Appl
7	1776	92.9	428	15	US-10-115-479-70	Sequence 70, Appl
8	1716.5	89.8	423	14	US-10-379-836-2	Sequence 2, Appli
9	1528	80.0	422	14	US-10-379-836-18	Sequence 18, Appl
10	1499	78.4	422	14	US-10-379-836-16	Sequence 16, Appl
11	1407	73.6	322	15	US-10-115-479-64	Sequence 64, Appl
12	1361	71.2	354	15	US-10-115-479-66	Sequence 66, Appl
13	803.5	42.0	211	9	US-09-925-302-467	Sequence 467, App
14	803.5	42.0	211	10	US-09-925-302-467	Sequence 467, App
15	646	33.8	416	15	US-10-074-978A-269	Sequence 269, App
16	641	33.5	417	15	US-10-074-978A-267	Sequence 267, App
17	641	33.5	417	15	US-10-074-978A-268	Sequence 268, App
18	641	33.5	417	16	US-10-477-515-3	Sequence 3, Appli
19	631.5	33.0	402	14	US-10-379-836-20	Sequence 20, Appl
20	627	32.8	416	15	US-10-074-978A-270	Sequence 270, App
21	623	32.6	716	9	US-09-910-059-125	Sequence 125, App
22	621.5	32.5	416	15	US-10-074-978A-266	Sequence 266, App
23	619.5	32.4	417	14	US-10-229-546-2	Sequence 2, Appli
24	619.5	32.4	417	14	US-10-229-546-9	Sequence 9, Appli
25	619.5	32.4	417	14	US-10-341-434-188	Sequence 188, App
26	619.5	32.4	417	15	US-10-262-511-72	Sequence 72, Appl
27	604	31.6	434	16	US-10-477-515-2	Sequence 2, Appli
28	604	31.6	437	13	US-10-200-344-10	Sequence 10, Appl
29	604	31.6	437	14	US-10-274-639-12	Sequence 12, Appl
30	604	31.6	437	15	US-10-333-574-12	Sequence 12, Appl
31	602	31.5	437	17	US-10-757-262-128	Sequence 128, App
32	563	29.5	374	9	US-09-888-615-61	Sequence 61, Appl
33	563	29.5	444	14	US-10-176-306-74	Sequence 74, Appl
34	546	28.6	399	14	US-10-200-910-8	Sequence 8, Appli
35	546	28.6	399	17	US-10-843-130-8	Sequence 8, Appli
36	543	28.4	613	9	US-09-910-059-113	Sequence 113, App
37	543	28.4	613	16	US-10-608-710-4	Sequence 4, Appli
38	533.5	27.9	419	15	US-10-072-012-788	Sequence 788, App
39	528.5	27.7	350	13	US-10-200-344-12	Sequence 12, Appl
40	522	27.3	286	15	US-10-072-012-887	Sequence 887, App
41	519.5	27.2	419	15	US-10-257-174-40	Sequence 40, Appl
42	519.5	27.2	436	14	US-10-200-910-6	Sequence 6, Appli
43	519.5	27.2	436	15	US-10-072-012-316	Sequence 316, App
44	519.5	27.2	436	15	US-10-072-012-784	Sequence 784, App
45	519.5	27.2	436	15	US-10-257-174-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 95.1%; Score 1817; DB 9; Length 386;
Best Local Similarity 98.6%; Pred. No. 1e-169;
Matches 341; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180
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Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
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Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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Db        301 SEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 2
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-212-877-2

  Query Match             95.1%;  Score 1817;  DB 14;  Length 386;
  Best Local Similarity   98.6%;  Pred. No. 1e-169;
  Matches  341;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              ||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||:| ||||||||||||||||||||||||||||||||||
Db        301 SEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-836-17

  Query Match             94.2%;  Score 1799.5;  DB 14;  Length 423;
  Best Local Similarity   89.6%;  Pred. No. 6.1e-168;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
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Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH----------------------------------------NRMWRK 203
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Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
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Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
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Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
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Db        361 TLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

  Query Match             93.6%;  Score 1788.5;  DB 9;  Length 423;
  Best Local Similarity   89.0%;  Pred. No. 7.3e-167;
  Matches  341;  Conservative    1;  Mismatches    4;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
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Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||                                   ||||||
Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
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Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              ||||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
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Db        361 TLYLAPGGGDDWIYDLGIKYSFT 383
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RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Query Match 93.6%; Score 1788.5; DB 14; Length 423;
Best Local Similarity 89.0%; Pred. No. 7.3e-167;
Matches 341; Conservative 1; Mismatches 4; Indels 37; Gaps 1;

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Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||                                   ||||||
Db        181 HAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
              ||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        241 NRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              ||||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        301 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||||||||||||||||||
Db        361 TLYLAPGGGDDWIYDLGIKYSFT 383
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RESULT 6
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match 92.9%; Score 1776; DB 15; Length 428;
Best Local Similarity 87.9%; Pred. No. 1.3e-165;

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  Matches  341;  Conservative    1;  Mismatches    4;  Indels   42;  Gaps    2;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIW 175
              |||||||||||||||||||||||||||||||||||||||||     |||||| ||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIW 180

Qy        176 IDCGIHAREWISPAFCLWFIGH-----------------------------------N 198
              |||||||||||||||||||||                                   |
Db        181 IDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKN 240

Qy        199 RMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASF 258
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        241 RMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASF 300

Qy        259 LRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTH 318
              |||||||||||||||||||||||||||||||||||||||||||||||||:| ||||||||
Db        301 LRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTH 360

Qy        319 GHGSETLYLAPGGGDDWIYDLGIKYSFT 346
              ||||||||||||||||||||||||||||
Db        361 GHGSETLYLAPGGGDDWIYDLGIKYSFT 388


RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-70

  Query Match             92.9%;  Score 1776;  DB 15;  Length 428;
  Best Local Similarity   87.9%;  Pred. No. 1.3e-165;
  Matches  341;  Conservative    1;  Mismatches    4;  Indels   42;  Gaps    2;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIW 175
              |||||||||||||||||||||||||||||||||||||||||     |||||| ||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIW 180

Qy        176 IDCGIHAREWISPAFCLWFIGH-----------------------------------N 198
              |||||||||||||||||||||                                   |
Db        181 IDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKN 240

Qy        199 RMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASF 258
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        241 RMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASF 300

Qy        259 LRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTH 318
              |||||||||||||||||||||||||||||||||||||||||||||||||:| ||||||||
Db        301 LRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTH 360

Qy        319 GHGSETLYLAPGGGDDWIYDLGIKYSFT 346
              ||||||||||||||||||||||||||||
Db        361 GHGSETLYLAPGGGDDWIYDLGIKYSFT 388


RESULT 8
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 423
;   TYPE: PRT
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;   ORGANISM: Papio hamadryas
US-10-379-836-2

  Query Match             89.8%;  Score 1716.5;  DB 14;  Length 423;
  Best Local Similarity   85.4%;  Pred. No. 8.9e-160;
  Matches  327;  Conservative    7;  Mismatches   12;  Indels   37;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              || |||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIEKKKQVHFFVNSSDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||| |||::|||||||||||:||:||||||||||||||:||||||
Db        121 EQYHSLNEIYSWIELITEKYPDMLTKIHIGSSYEKHPLYVLKVSGKEQTAKNAMWIDCGI 180

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||                                   ||||||
Db        181 HAREWISPAFCLWFIGHITEYYGIIGEYTNLLRHVDFYVMPVVNVDGYDYSWKKNRMWRK 240

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
              |||||||| ||||||| || |||||||||||| |||||||||||||||| ||||:||||||
Db        241 NRSFYANNRCIGTDLNRNFASKHWCEEGASSFSCSETYCGLYPESEPEAKAVANFLRRNI 300

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              | |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||
Db        301 NHIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIQKTSKNIRYTHGRGSE 360

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||| ||||||||||||||
Db        361 TLYLAPGGADDWIYDLGIKYSFT 383


RESULT 9
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-379-836-18

  Query Match             80.0%;  Score 1528;  DB 14;  Length 422;
  Best Local Similarity   76.2%;  Pred. No. 3.1e-141;
  Matches  292;  Conservative   24;  Mismatches   29;  Indels   38;  Gaps    2;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              |||  | :|| |:|: ||| |||||||||:||||||||:|||||||:||||||||:
Db          1 MKLHGLGILVAIILY-EQHGFAFQSGQVLSALPRTSRQVQLLQNLTTTYEVVLWQPVTAE 59

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               | |||:||||||||||:|||||||| || :|: :|||||:||  ||||||||||||
Db         60 FIEKKKEVHFFVNASDVDSVKAHLNVSRIPFNVLMNNVEDLIEQQTFNDTVSPRASASYY 119

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||| |||:|||||| ||:||||||||||||||||  ||||||||||
Db        120 EQYHSLNEIYSWIEVITEQHPDMLQKIYIGSSFEKYPLYVLKVSGKEQRIKNAIWIDCGI 179

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||:                                   ||||||
Db        180 HAREWISPAFCLWFIGYVTQFHGKENLYTRLLRHVDFYIMPVMNVDGYDYTWKKNRMWRK 239

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
              ||| : || |:||||| || ||||||:|||||||||||||||||||||||| ||||||
Db        240 NRSAHKNNRCVGTDLNRNFASKHWCEKGASSSSCSETYCGLYPESEPEVKAVADFLRRNI 299

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              : |||||||||||| |:||||| |||||||||||||||||||:  :|||||||| |||
Db        300 DHIKAYISMHSYSQQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSE 359

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              :||||||| ||||||||||||||
Db        360 SLYLAPGGSDDWIYDLGIKYSFT 382


RESULT 10
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-379-836-16

  Query Match             78.4%;  Score 1499;  DB 14;  Length 422;
  Best Local Similarity   74.7%;  Pred. No. 2.2e-138;
  Matches  286;  Conservative   26;  Mismatches   33;  Indels   38;  Gaps    2;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              |||  | ||| |:|: |:|  ||||| ||:||||||||:|||||||:||||||:
Db          1 MKLYGLGVLVAIILY-EKHGLAFQSGHVLSALPRTSRQVQLLQNLTTTYEVVLWQPVTAE 59

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               | |||:||||||||::|||:|| | || :||: :|||||||| ||||||||:|||
Db         60 FIEKKKEVHFFVNASDVNSVKAYLNASRIPFNVLMNNVEDLIQQQTSNDTVSPRASSSYY 119

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||| |||:||||| ||:||||:|||||||||||   ||||||||||
Db        120 EQYHSLNEIYSWIEVITEQHPDMLQKIYIGSSYEKYPLYVLKVSGKEHRVKNAIWIDCGI 179

Qy        181 HAREWISPAFCLWFIGH-----------------------------------NRMWRK 203
              |||||||||||||||||:                                   ||||||
Db        180 HAREWISPAFCLWFIGYVTQFHGKENTYTRLLRHVDFYIMPVMNVDGYDYTWKKNRMWRK 239

Qy        204 NRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNI 263
              ||| : || |:||||| || ||||||:|||| |||||||||||||||||||| ||||||
Db        240 NRSVHMNNRCVGTDLNRNFASKHWCEKGASSFSCSETYCGLYPESEPEVKAVADFLRRNI 299

Qy        264 NQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323
              | |||||||||||| |:||||| |||||||||||||||||||:  :|||||||| |||
Db        300 NHIKAYISMHSYSQQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSE 359

Qy        324 TLYLAPGGGDDWIYDLGIKYSFT 346
              :||||||| ||||||||||||||
Db        360 SLYLAPGGSDDWIYDLGIKYSFT 382


RESULT 11
US-10-115-479-64
```

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; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-64

  Query Match             73.6%;  Score 1407;  DB 15;  Length 322;
  Best Local Similarity   80.6%;  Pred. No. 1.6e-129;
  Matches  279;  Conservative    1;  Mismatches    2;  Indels   64;  Gaps    1;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWID--- 177

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240

Db        178 ------------------------------------------------------------ 177

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        178 -CGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 236

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
              |||||||:| ||||||||||||||||||||||||||||||||||||
Db        237 SEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 282


RESULT 12
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
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;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-66

  Query Match            71.2%;  Score 1361;  DB 15;  Length 354;
  Best Local Similarity  69.3%;  Pred. No. 6.3e-125;
  Matches  269;  Conservative    0;  Mismatches    3;  Indels  116;  Gaps    3;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIW 175
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Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIW 180

Qy        176 IDCGIHAREWISPAFCLWFIGH-----------------------------------N 198
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Db        181 IDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKN 240

Qy        199 RMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASF 258
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Qy        259 LRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTH 318

Db        290 ---------------------------------------------------------- 289

Qy        319 GHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

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  Best Local Similarity  88.8%;  Pred. No. 2e-70;
  Matches  151;  Conservative    2;  Mismatches    8;  Indels    9;  Gaps    2;

Qy        185 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSS 236
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Db          3 WIS-MLCRWLMWMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 61

Qy        237 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        297 SLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

  Query Match            42.0%;  Score 803.5;  DB 10;  Length 211;
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Qy        185 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSS 236
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Qy        237 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 296
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Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        297 SLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346
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Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
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;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-10-074-978A-269

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Qy         62 IVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYE 121
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Qy        122 QYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIH 181
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Qy        182 AREWISPAFCLWFI------------------------------GH------NRMWRKN 204
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Qy        205 RSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNIN 264
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Qy        265 QIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSET 324
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Db        296 SIKAYLTIHSYSQMILYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGATT 354

Qy        325 LYLAPGGGDDWIYDLGIKYSFT 346
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Job time : 83.3729 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:35:31 ; Search time 333.305 Seconds
(without alignments)
1196.740 Million cell updates/sec

Title: US-09-980-881A-2
Perfect score: 1911
Sequence: 1 MKLCSLAVLVPIVLFCEQHV.....IKYSFTSNPPVEKLLPLSLK 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1911	100.0	360	25	US-09-980-881A-2	Sequence 2, Appli
3	1886	98.7	360	27	US-10-170-205E-13306	Sequence 13306, A
4	1886	98.7	360	34	US-10-803-180-126	Sequence 126, App
5	1886	98.7	360	35	US-10-918-754-1941	Sequence 1941, Ap
6	1886	98.7	360	36	US-60-452-680-21530	Sequence 21530, A
7	1886	98.7	360	36	US-60-453-050-13037	Sequence 13037, A
8	1886	98.7	360	36	US-60-453-135-13037	Sequence 13037, A
9	1886	98.7	360	36	US-60-455-444-6989	Sequence 6989, Ap
10	1886	98.7	360	36	US-60-465-241-6989	Sequence 6989, Ap
11	1886	98.7	360	36	US-60-466-412-13037	Sequence 13037, A
12	1886	98.7	360	36	US-60-495-114-1941	Sequence 1941, Ap
13	1886	98.7	366	24	US-09-949-003C-3190	Sequence 3190, Ap
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16	1884	98.6	360	24	US-09-949-003C-2616	Sequence 2616, Ap
17	1818	95.1	386	1	PCT-US03-31531-18	Sequence 18, Appl
18	1817	95.1	386	1	PCT-US02-08289-2	Sequence 2, Appli
19	1817	95.1	386	28	US-10-212-877-2	Sequence 2, Appli
20	1799.5	94.2	423	1	PCT-US03-26773-2	Sequence 2, Appli
21	1799.5	94.2	423	3	US-07-959-944A-3	Sequence 3, Appli
22	1799.5	94.2	423	22	US-09-791-537-96834	Sequence 96834, A
23	1799.5	94.2	423	24	US-09-949-003C-2062	Sequence 2062, Ap
24	1799.5	94.2	423	29	US-10-379-836-17	Sequence 17, Appl
25	1799.5	94.2	423	30	US-10-486-034-2	Sequence 2, Appli
26	1799.5	94.2	423	36	US-60-353-790-3726	Sequence 3726, Ap
27	1799.5	94.2	423	36	US-60-361-523-17	Sequence 17, Appl
28	1794.5	93.9	423	27	US-10-170-205E-13305	Sequence 13305, A
29	1794.5	93.9	423	34	US-10-803-180-127	Sequence 127, App
30	1794.5	93.9	423	35	US-10-918-754-1942	Sequence 1942, Ap
31	1794.5	93.9	423	36	US-60-452-680-21529	Sequence 21529, A
32	1794.5	93.9	423	36	US-60-453-050-13036	Sequence 13036, A
33	1794.5	93.9	423	36	US-60-453-135-13036	Sequence 13036, A
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35	1794.5	93.9	423	36	US-60-465-241-6988	Sequence 6988, Ap
36	1794.5	93.9	423	36	US-60-466-412-13036	Sequence 13036, A
37	1794.5	93.9	423	36	US-60-495-114-1942	Sequence 1942, Ap
38	1794.5	93.9	429	24	US-09-949-003C-3188	Sequence 3188, Ap
39	1794.5	93.9	429	24	US-09-949-003C-3189	Sequence 3189, Ap
40	1788.5	93.6	423	1	PCT-US02-08289-4	Sequence 4, Appli
41	1788.5	93.6	423	28	US-10-212-877-4	Sequence 4, Appli
42	1786.5	93.5	424	22	US-09-760-475-1824	Sequence 1824, Ap
43	1786.5	93.5	424	28	US-10-227-425-1824	Sequence 1824, Ap
44	1785	93.4	338	25	US-09-980-881-3	Sequence 3, Appli
45	1785	93.4	338	25	US-09-980-881A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-980-881-2
; Sequence 2, Application US/09980881
; GENERAL INFORMATION:
; APPLICANT: AKIRA MATSUMOTO
; TITLE OF INVENTION: Human Brain Carboxypeptidase B
; FILE REFERENCE: MAT-101PCT
; CURRENT APPLICATION NUMBER: US/09/980,881
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: JP 1999-125169
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-980-881-2

Query Match 100.0%; Score 1911; DB 25; Length 360;

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Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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RESULT 2
US-09-980-881A-2
; Sequence 2, Application US/09980881A
; GENERAL INFORMATION:
;  APPLICANT: AKIRA MATSUMOTO
;  TITLE OF INVENTION: Human Brain Carboxypeptidase B
;  FILE REFERENCE: MAT-101PCT
;  CURRENT APPLICATION NUMBER: US/09/980,881A
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: JP   1999-125169
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-980-881A-2

  Query Match             100.0%;  Score 1911;  DB 25;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-192;
  Matches  360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360


RESULT 3
US-10-170-205E-13306
; Sequence 13306, Application US/10170205E
; GENERAL INFORMATION:
;  APPLICANT: ADAMS, Mark
;  TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
;  TITLE OF INVENTION:  CAPTURE AGENTS, AND USES THEREOF
;  FILE REFERENCE: CL001381
;  CURRENT APPLICATION NUMBER: US/10/170,205E
;  CURRENT FILING DATE:  2002-06-13
;  NUMBER OF SEQ ID NOS: 40312
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13306
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-170-205E-13306

  Query Match             98.7%;  Score 1886;  DB 27;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 4
US-10-803-180-126
; Sequence 126, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-803-180-126

  Query Match             98.7%;  Score 1886;  DB 34;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                 |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                 |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                 |||||||:||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 5
US-10-918-754-1941
; Sequence 1941, Application US/10918754
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001480
;  CURRENT APPLICATION NUMBER: US/10/918,754
;  CURRENT FILING DATE:  2004-08-16
;  NUMBER OF SEQ ID NOS: 91238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1941
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-918-754-1941

  Query Match             98.7%;  Score 1886;  DB 35;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                 |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                 |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                 |||||||:||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 6
US-60-452-680-21530
; Sequence 21530, Application US/60452680
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  GRUPE, Andrew
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001450
;  CURRENT APPLICATION NUMBER: US/60/452,680
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 116213
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21530
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-452-680-21530

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                 |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                 |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                 |||||||:||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 7
US-60-453-050-13037
; Sequence 13037, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-050-13037

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
               |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
               |||||||:|||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 8
US-60-453-135-13037
; Sequence 13037, Application US/60453135
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-135-13037

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
               |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
               |||||||:|||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 9
US-60-455-444-6989
; Sequence 6989, Application US/60455444
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  BEGOVICH, Ann
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001455
;  CURRENT APPLICATION NUMBER: US/60/455,444
;  CURRENT FILING DATE:  2003-03-18
;  NUMBER OF SEQ ID NOS: 50986
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-455-444-6989

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
               |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
               |||||||:|||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 10
US-60-465-241-6989
; Sequence 6989, Application US/60465241
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  BEGOVICH, Ann
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001468
;  CURRENT APPLICATION NUMBER: US/60/465,241
;  CURRENT FILING DATE:  2003-04-23
;  NUMBER OF SEQ ID NOS: 258418
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-465-241-6989

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                |||||||:|||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 11
US-60-466-412-13037
; Sequence 13037, Application US/60466412
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001466
;  CURRENT APPLICATION NUMBER: US/60/466,412
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 429241
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-466-412-13037

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                |||||||:|||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 12
US-60-495-114-1941
; Sequence 1941, Application US/60495114
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001480
;  CURRENT APPLICATION NUMBER: US/60/495,114
;  CURRENT FILING DATE:  2003-08-15
;  NUMBER OF SEQ ID NOS: 91238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1941
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-495-114-1941

  Query Match             98.7%;  Score 1886;  DB 36;  Length 360;
  Best Local Similarity   98.6%;  Pred. No. 9.9e-190;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
                |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db         181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy         301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
                |||||||:|||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 13
US-09-949-003C-3190
; Sequence 3190, Application US/09949003C
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
;  TITLE OF INVENTION:  DISORDERS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000791
;  CURRENT APPLICATION NUMBER: US/09/949,003C
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,446
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 74065
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3190
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-949-003C-3190

  Query Match             98.7%;  Score 1886;  DB 24;  Length 366;
  Best Local Similarity   98.6%;  Pred. No. 1e-189;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           7 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 66

Qy          61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
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Db         67 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 126

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        127 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 186

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db        187 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 246

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Db        247 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 306

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
              |||||||:|||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        307 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 366


RESULT 14
US-09-949-003C-3191
; Sequence 3191, Application US/09949003C
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
;  TITLE OF INVENTION:  DISORDERS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000791
;  CURRENT APPLICATION NUMBER: US/09/949,003C
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,446
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 74065
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3191
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-949-003C-3191

  Query Match            98.7%;  Score 1886;  DB 24;  Length 366;
  Best Local Similarity  98.6%;  Pred. No. 1e-189;
  Matches  355;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
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Db          7 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 66

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 126

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        127 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 186

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db        187 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 246

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
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Db        247 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 306

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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RESULT 15
US-09-791-537-142876
; Sequence 142876, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142876
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-142876

  Query Match            98.6%;  Score 1884;  DB 22;  Length 360;
  Best Local Similarity  98.3%;  Pred. No. 1.6e-189;
  Matches  354;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MKLCSLAVLVPIVLFCEQHVFAFQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db          1 MKLCSLAVLVPIVLFCEQHVFAFQTGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTAD 60

Qy         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LIVKKKQVHFFVNASDVDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYY 120

Qy        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGI 180

Qy        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCEEGASSSSCSET 240
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db        181 HAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSET 240

Qy        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVA 300

Qy        301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
              |||||||:| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: October 28, 2004, 20:01:43
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 03:40:54 ; Search time 104.873 Seconds
(without alignments)
2439.944 Million cell updates/sec

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Perfect score: 1911
Sequence: 1 MKLCSLAVLVPIVLFCEQHV.....IKYSFTSNPPVEKLLPLSLK 360

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Maximum Match 100%
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SUMMARIES

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1	1849.5	96.8	1625	4	US-09-813-133A-1	Sequence 1, Appli
2	1832	95.9	1272	2	US-08-869-057-1	Sequence 1, Appli
3	1832	95.9	1749	1	US-07-649-591B-2	Sequence 2, Appli
4	1832	95.9	1749	1	US-08-277-540-2	Sequence 2, Appli
5	1832	95.9	1749	1	US-08-430-787A-2	Sequence 2, Appli
6	640.5	33.5	1215	1	US-08-696-139-1	Sequence 1, Appli
7	639	33.4	1263	2	US-08-860-882A-56	Sequence 56, Appl
8	639	33.4	1263	4	US-09-011-769A-38	Sequence 38, Appl
9	631.5	33.0	1284	2	US-08-860-882A-71	Sequence 71, Appl
10	631.5	33.0	1284	4	US-09-011-769A-55	Sequence 55, Appl
11	623	32.6	2154	3	US-09-171-945-124	Sequence 124, App
12	619.5	32.4	1622	4	US-09-023-655-1020	Sequence 1020, Ap
13	611.5	32.0	1311	4	US-09-675-305-9	Sequence 9, Appli
14	611.5	32.0	1311	4	US-10-200-344-9	Sequence 9, Appli
15	604	31.6	927	2	US-08-782-760-5	Sequence 5, Appli
16	604	31.6	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	576	30.1	921	1	US-08-696-139-3	Sequence 3, Appli
18	564	29.5	2128	4	US-09-675-305-13	Sequence 13, Appl
19	564	29.5	2128	4	US-10-200-344-13	Sequence 13, Appl
20	561	29.4	999	2	US-08-860-882A-67	Sequence 67, Appl
21	561	29.4	999	4	US-09-011-769A-50	Sequence 50, Appl
22	561	29.4	1053	2	US-08-860-882A-64	Sequence 64, Appl
23	561	29.4	1053	4	US-09-011-769A-46	Sequence 46, Appl
24	554	29.0	1053	4	US-09-463-451-27	Sequence 27, Appl
c 25	554	29.0	1053	4	US-09-463-451-28	Sequence 28, Appl
26	554	29.0	1059	2	US-08-860-882A-74	Sequence 74, Appl
27	554	29.0	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	553	28.9	1059	2	US-08-860-882A-77	Sequence 77, Appl
29	553	28.9	1059	4	US-09-011-769A-63	Sequence 63, Appl
30	546	28.6	1200	4	US-09-710-099-7	Sequence 7, Appli
31	546	28.6	1200	4	US-10-200-910-7	Sequence 7, Appli
32	543	28.4	1870	3	US-09-171-945-112	Sequence 112, App
33	528.5	27.7	1050	4	US-09-675-305-11	Sequence 11, Appl
34	528.5	27.7	1050	4	US-10-200-344-11	Sequence 11, Appl
35	519.5	27.2	1311	4	US-09-710-099-5	Sequence 5, Appli
36	519.5	27.2	1311	4	US-10-200-910-5	Sequence 5, Appli
37	513	26.8	1251	3	US-08-640-906-3	Sequence 3, Appli
38	513	26.8	1251	3	US-09-395-936-3	Sequence 3, Appli
39	487.5	25.5	1257	3	US-08-640-906-1	Sequence 1, Appli
40	487.5	25.5	1257	3	US-09-395-936-1	Sequence 1, Appli
41	460.5	24.1	945	4	US-09-710-099-3	Sequence 3, Appli
42	460.5	24.1	945	4	US-09-710-099-11	Sequence 11, Appl
43	460.5	24.1	945	4	US-10-200-910-3	Sequence 3, Appli
44	460.5	24.1	945	4	US-10-200-910-11	Sequence 11, Appl
45	458.5	24.0	2247	4	US-09-710-099-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

Pred. No.:	6.66e-227	Length:	1625
Score:	1849.50	Matches:	355
Percent Similarity:	94.18%	Conservative:	1
Best Local Similarity:	93.92%	Mismatches:	4
Query Match:	96.78%	Indels:	18
DB:	4	Gaps:	1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

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Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
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Db         17 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 76

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
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Db         77 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 136

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 196

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 256

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGATGTGGAAGAT 316

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 376

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 436

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 496

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              |||||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db        497 TTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGACTGTGGAATC 556

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 616

Qy        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 676

Qy        221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240
              ||||||    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 736

Qy        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 796

Qy        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 856

Qy        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 916

Qy        301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
              ||||||||||||||||||:::|||    ||||||||||||||||||||||||||||||||||
Db        917 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 976

Qy        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1036

Qy        341 IleLysTyrSerPhe---------------------------------------------- 345
              |||||||||||||||
Db       1037 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1096

Qy        346 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                    ||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1148

RESULT 2
US-08-869-057-1
; Sequence 1, Application US/08869057
```

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; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    PUBLICATION INFORMATION:
;      AUTHORS:  Eaton, Dan L.
;      AUTHORS:  Malloy, Beth E.
;      AUTHORS:  Tsai, Siao P
;      AUTHORS:  Henzel, William
;      AUTHORS:  Drayna, Dennis
;      TITLE:  Isolation, Molecular Cloning, and Partial
;      TITLE:  Characterization of a No. 5985562el Carboxypeptidase B
;      TITLE:  from Human Plasma
;      JOURNAL:  J. Biol. Chem.
;      VOLUME:  266
;      ISSUE:  32
;      PAGES:  21833-21838
;      DATE:  No. 5985562 15-1991
US-08-869-057-1

Alignment Scores:
Pred. No.:              7.69e-225       Length:         1272
Score:                  1832.00         Matches:        357
Percent Similarity:     86.27%          Conservative:   1
Best Local Similarity:  86.02%          Mismatches:     2
Query Match:            95.87%          Indels:         55
DB:                     2               Gaps:           2

US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 60

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 120

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal  80
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Db        181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 240

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 300

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 360

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 420

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 480

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 540

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 600

Qy        197 ------------------------------------------------------------ 197

Db        601 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 660

Qy        198 ----------------------------------------AsnArgMetTrpArgLys 203
                                                     ||||||||||||||||
Db        661 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 720

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCT 780

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 840

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 900

Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 960

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1020

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
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Db       1021 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1080

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1140

Qy        344 SerPhe-----------------------------------------------------Th 346
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Db       1141 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1200

Qy        346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
              |||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1243
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```
RESULT 3
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  hybridization probe
;      LOCATION:  133 to 178
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  potential clip site
;      LOCATION:  380 to 382
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  signal sequence
;      LOCATION:  41 to 106
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-07-649-591B-2

Alignment Scores:
Pred. No.:              1.34e-224       Length:         1749
Score:                  1832.00         Matches:        357
Percent Similarity:     86.27%          Conservative:   1
Best Local Similarity:  86.02%          Mismatches:     2
Query Match:            95.87%          Indels:         55
DB:                     1               Gaps:           2

US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 100
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Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 160

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 280

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 340

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 400

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 520

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 580

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 640

Qy        197 ------------------------------------------------------------ 197

Db        641 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700

Qy        198 ----------------------------------------AsnArgMetTrpArgLys 203
                                                     ||||||||||||||||||
Db        701 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 760

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCT 820

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 880

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 940

Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 1000

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1060

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1120

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1180

Qy        344 SerPhe----------------------------------------------------Th 346

              ||||||                                                  ||
Db       1181 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1240

Qy        346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
               ||||||||||||||||||||||||||||||||||||||||||
Db       1241 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

RESULT 4
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-277-540-2

Alignment Scores:
Pred. No.:                1.34e-224       Length:          1749
Score:                    1832.00         Matches:         357
Percent Similarity:       86.27%          Conservative:    1
Best Local Similarity:    86.02%          Mismatches:      2
Query Match:              95.87%          Indels:          55
DB:                       1               Gaps:            2

US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 100

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 160
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Qy        41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy        61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       221 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 280

Qy        81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       281 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 340

Qy       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       341 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 400

Qy       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460

Qy       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       461 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 520

Qy       161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       521 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 580

Qy       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       581 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 640

Qy       197 ------------------------------------------------------------ 197

Db       641 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700

Qy       198 ----------------------------------------AsnArgMetTrpArgLys 203
                                                       ||||||||||||||||
Db       701 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 760

Qy       204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       761 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCT 820

Qy       224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       821 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 880

Qy       244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       881 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 940

Qy       264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       941 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 1000

Qy       284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1001 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1060

Qy       304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
             ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db      1061 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1120

Qy       324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1121 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1180

Qy       344 SerPhe-------------------------------------------------------Th 346
             ||||||                                                       ||
Db      1181 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1240

Qy       346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
             ||||||||||||||||||||||||||||||||||||||||||||
Db      1241 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

RESULT 5
US-08-430-787A-2
; Sequence 2, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-787A-2

Alignment Scores:
Pred. No.:              1.34e-224      Length:          1749
Score:                  1832.00        Matches:         357
Percent Similarity:     86.27%         Conservative:    1
Best Local Similarity:  86.02%         Mismatches:      2
Query Match:            95.87%         Indels:          55
DB:                     1              Gaps:            2

US-09-980-881A-2 (1-360) x US-08-430-787A-2 (1-1749)

Qy         1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        41 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 100

Qy        21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 160
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Qy        41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy        61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       221 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 280

Qy        81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       281 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 340

Qy       101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       341 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 400

Qy       121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460

Qy       141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       461 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 520

Qy       161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       521 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 580

Qy       181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       581 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 640

Qy       197 ------------------------------------------------------------ 197

Db       641 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700

Qy       198 -----------------------------------------AsnArgMetTrpArgLys 203
                                                       ||||||||||||||||
Db       701 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 760

Qy       204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
             ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db       761 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCT 820

Qy       224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       821 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 880

Qy       244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       881 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 940

Qy       264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       941 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 1000

Qy       284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1001 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1060

Qy       304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
             ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db      1061 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1120

Qy       324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1121 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1180

Qy       344 SerPhe-------------------------------------------------------Th 346
             ||||||                                                       ||
Db      1181 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1240

Qy       346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
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             ||||||||||||||||||||||||||||||||||||||||||||
Db      1241 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

RESULT 6
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1215 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1215
US-08-696-139-1

Alignment Scores:
Pred. No.:              7.49e-72        Length:         1215
Score:                  640.50          Matches:        136
Percent Similarity:     54.29%          Conservative:   60
Best Local Similarity:  37.67%          Mismatches:     122
Query Match:            33.52%          Indels:         43
DB:                     1               Gaps:           6

US-09-980-881A-2 (1-360) x US-08-696-139-1 (1-1215)

Qy         23 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 42
              |||:::      :::|||                          :::   :::|||
Db         28 TTCGAAGGGGAGAAGGTGTTCCGTGTCAATGTTGAAGATGAAAATGACATCAGCTTACTC 87

Qy         43 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62
                    |||   :::|||   :::|||      |||:::|||   :::         |||
Db         88 CATGAGTTGGCCAGCACCAGGCAGATTGACTTCTGGAAACCAGATTCTGTCACACAAATC 147
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Qy         63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82
Db        148 AAACCTCACAGTACAGTTGACTTCCGTGTGAAAGCAGAAGATATTTTGGCTGTGGAAGAC 207

Qy         83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102
Db        208 TTTCTGGAGCAGAATGAACTACAATATGAGGTACTCATAAACAACCTGAGATCTGTGCTC 267

Qy        103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122
Db        268 GAGGCTCAGTTTGACAGCAGAGTC---------CGTACAACTGGACACAGTTATGAGAAG 318

Qy        123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142
Db        319 TACAACAACTGGGAAACGATCGAGGCTTGGACTAAGCAAGTCACCAGTGAAAATCCAGAC 378

Qy        143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162
Db        379 CTCATCTCTCGCACAGCCATCGGAACTACATTTTTAGGAAACAATATATACCTCCTCAAG 438

Qy        163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
Db        439 GTT---GGCAAACCTGGACCAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 495

Qy        183 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------------------- 195
Db        496 AGAGAATGGATTTCCCATGCATTTTGCCAGTGGTTTGTGAGAGAGGCTGTTCTCACCTAT 555

Qy        195 ---------------------------------------------------------- 195
Db        556 GGATATGAGAGTCACATGACAGAATTCCTCAACAAGCTAGACTTTTATGTCTTGCCTGTG 615

Qy        196 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 205
Db        616 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGAAAGACCCGC 675

Qy        206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
Db        676 TCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 732

Qy        226 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245
Db        733 GGGTGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGCT 792

Qy        246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 265
Db        793 GCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAACCTCTCCTCC 852

Qy        266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285
Db        853 ATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCTTATTCCTAT 912

Qy        286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 305
Db        913 GATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCTGCCGTGAAA 972

Qy        306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325
Db        973 GAACTT---GCTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCTACAACAATC 1029

Qy        326 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345
Db       1030 TATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAATATTCCTTC 1089

Qy        346 Thr 346
Db       1090 ACC 1092
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RESULT 7
US-08-860-882A-56
; Sequence 56, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM,JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-860-882A-56

Alignment Scores:

Pred. No.:	1.25e-71	Length:	1263
Score:	639.00	Matches:	135
Percent Similarity:	53.83%	Conservative:	69
Best Local Similarity:	35.62%	Mismatches:	131
Query Match:	33.44%	Indels:	44
DB:	2	Gaps:	7

US-09-980-881A-2 (1-360) x US-08-860-882A-56 (1-1263)

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Qy          6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24
Db          4 CTCTTGGTTCTGGTGACTGTGGCCCTGGCATCTGCTCATCATGGTGGTGAGCACTTTGAA 63

Qy         25 SerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44
Db         64 GGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATCCGCGAG 123

Qy         45 LeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64
Db        124 TTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATCAAACCT 183

Qy         65 LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAlaHisLeu 84
Db        184 CACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAATGTTCTA 243

Qy         85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIleGlnGln 104
Db        244 AAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTGGAGGCT 303
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Qy        105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db        304 CAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAGTACAAC 354

Qy        125 SerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAspMetLeu 144
Db        355 AAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCCCTCATC 414

Qy        145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164
Db        415 TCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAGGTT--- 471

Qy        165 GlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGlu 184
Db        472 GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCCAGAGAG 531

Qy        185 TrpIleSerProAlaPheCysLeuTrpPheIle-------------------------- 195
Db        532 TGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTATGGACGT 591

Qy        195 ------------------------------------------------------------ 195
Db        592 GAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTGCTCAAT 651

Qy        196 ------GlyHis-----------------AsnArgMetTrpArgLysAsnArgSerPhe 207
Db        652 ATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGCTCCACC 711

Qy        208 TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLysHisTrp 227
Db        712 CATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCTGGTTGG 768

Qy        228 CysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db        769 TGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCCGCAGAG 828

Qy        248 SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267
Db        829 TCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCCATCAAG 888

Qy        268 AlaTyrIleSerMetHisSerTyrSerGlnHisIleValProProTyrSerTyrThrArg 287
Db        889 GCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATATGCTTAC 948

Qy        288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
Db        949 AAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAAGAACTT 1008

Qy        308 AspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
Db       1009 ---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATCTATCCT 1065

Qy        328 AlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 346
Db       1066 GCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTCACC 1122
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RESULT 8
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

Alignment Scores:

Pred. No.:	1.25e-71	Length:	1263
Score:	639.00	Matches:	135
Percent Similarity:	53.83%	Conservative:	69
Best Local Similarity:	35.62%	Mismatches:	131
Query Match:	33.44%	Indels:	44
DB:	4	Gaps:	7

US-09-980-881A-2 (1-360) x US-09-011-769A-38 (1-1263)

```
Qy          6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24
Db          4 CTCTTGGTTCTGGTGACTGTGGCCCTGGCATCTGCTCATCATGGTGGTGAGCACTTTGAA 63

Qy         25 SerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44
Db         64 GGCGAGAAGGTGTTCCGTGTTAACGTTCAAGATGAAAATCACATTAACATAATCCGCGAG 123

Qy         45 LeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64
Db        124 TTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATCAAACCT 183

Qy         65 LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAlaHisLeu 84
Db        184 CACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAATGTTCTA 243

Qy         85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIleGlnGln 104
Db        244 AAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTGGAGGCT 303

Qy        105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db        304 CAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAGTACAAC 354

Qy        125 SerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAspMetLeu 144
Db        355 AAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCCCTCATC 414

Qy        145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164
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Db        415 TCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAGGTT--- 471

Qy        165 GlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGlu 184
              |||||           |||   ||||||::::::|||||||   ||||||||||
Db        472 GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCCAGAGAG 531

Qy        185 TrpIleSerProAlaPheCysLeuTrpPheIle---------------------------- 195
              ||||||||||||||||||||   ||||||:::
Db        532 TGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTATGGACGT 591

Qy        195 ------------------------------------------------------------ 195

Db        592 GAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTGCTCAAT 651

Qy        196 -------GlyHis------------------AsnArgMetTrpArgLysAsnArgSerPhe 207
                    |||:::                 :::|||   |||||||   ||||||
Db        652 ATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGCTCCACC 711

Qy        208 TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLysHisTrp 227
              :::     :::   ||||||||||||||   |||   ||||||          |||
Db        712 CATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCTGGTTGG 768

Qy        228 CysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
              ||||||   |||||||||   :::   |||   ||||||||||||||          |||
Db        769 TGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCCGCAGAG 828

Qy        248 SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267
              ||||||   |||   ||||||:::|||   |||:::|||       ::::::   ||||||
Db        829 TCTGAAAAGGAAACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCCATCAAG 888

Qy        268 AlaTyrIleSerMetHisSerTyrSerGlnHisIleValProProTyrSerTyrThrArg 287
              ||||||:::::::::|||||||||||||||   :::::::::|||||||||||||
Db        889 GCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATATGCTTAC 948

Qy        288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
                    :::::::::   ||||||:::   :::|||          |||:::   :::
Db        949 AAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAAGAACTT 1008

Qy        308 AspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
                  :::         |||:::||||||:::|||   |||:::   |||:::|||
Db       1009 ---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATCTATCCT 1065

Qy        328 AlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 346
              |||   ||||||   |||||||||   ||||||   ||||||:::||||||||||||
Db       1066 GCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTCACC 1122

RESULT 9
US-08-860-882A-71
; Sequence 71, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-71

Alignment Scores:
Pred. No.:                1.18e-70        Length:          1284
Score:                    631.50          Matches:         129
Percent Similarity:       54.57%          Conservative:    68
Best Local Similarity:    35.73%          Mismatches:      121
Query Match:              33.05%          Indels:          43
DB:                       2               Gaps:            6

US-09-980-881A-2 (1-360) x US-08-860-882A-71 (1-1284)

Qy         23 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 42
              |||:::      :::|||                        :::   ::::::
Db         85 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 144

Qy         43 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62
              :::   |||   :::|||   :::|||      |||:::|||   :::          |||
Db        145 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 204

Qy         63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82
                        |||   |||   |||   |||   |||        |||:::
Db        205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 264

Qy         83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102
              |||      :::   :::         ||||||:::::::::::   :::::::::
Db        265 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324

Qy        103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122
              :::   |||      :::                |||||:::         ||||||:::
Db        325 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 375

Qy        123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142
              |||:::          |||   :::|||   :::   :::        :::|||
Db        376 TACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCC 435

Qy        143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162
              :::::::::::      ||||||:::::|||||         :::|||:::||||||
Db        436 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 495

Qy        163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
              |||   ||||||          |||   ||||||::::::|||||||   ||||||
Db        496 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 552

Qy        183 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------------------- 195
              ||||||||||||||||||||||||||   ||||||:::
Db        553 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 612

Qy        195 ------------------------------------------------------------ 195

Db        613 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 672

Qy        196 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 205
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                    |||:::                  :::|||   |||||||||   |||
Db        673 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 732

Qy        206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
              |||   :::      :::   ||||||||||||||   |||   ||||||
Db        733 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 789

Qy        226 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245
              |||||||||   |||||||||   :::   |||   ||||||||||||||||
Db        790 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 849

Qy        246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 265
              |||||||||   |||   ||||||:::|||   |||:::|||       ::::::
Db        850 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 909

Qy        266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 285
              ||||||||||:::::::::|||||||||||||||   :::::::::||||||||||||
Db        910 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 969

Qy        286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 305
                          :::::::::   ||||||:::   :::|||         |||:::
Db        970 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029

Qy        306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325
                :::      :::         |||:::||||||:::|||   |||:::   |||:::
Db       1030 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1086

Qy        326 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345
              |||   |||   ||||||   |||||||||   ||||||   |||||||:::|||||||||
Db       1087 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146

Qy        346 Thr 346
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Db       1147 ACC 1149

RESULT 10
US-09-011-769A-55
; Sequence 55, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;  INFORMATION FOR SEQ ID NO: 55:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1284 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION: 1..1272
;       FEATURE:
;            NAME/KEY:  mat_peptide
;            LOCATION: 352..1272
;       SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-55

Alignment Scores:
Pred. No.:              1.18e-70      Length:          1284
Score:                  631.50        Matches:         129
Percent Similarity:     54.57%        Conservative:    68
Best Local Similarity:  35.73%        Mismatches:      121
Query Match:            33.05%        Indels:          43
DB:                     4             Gaps:            6

US-09-980-881A-2 (1-360) x US-09-011-769A-55 (1-1284)

Qy         23 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 42
              |||:::    :::|||                                 :::   ::::::
Db         85 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 144

Qy         43 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62
              :::   |||   :::|||   :::|||      |||:::|||   :::        |||
Db        145 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 204

Qy         63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82
                           |||   |||   |||   |||   |||         |||:::
Db        205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 264

Qy         83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102
                 |||       :::   :::          ||||||:::::::::::   :::::::::
Db        265 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324

Qy        103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122
              :::   |||       :::                |||||:::         |||||:::
Db        325 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 375

Qy        123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142
              |||:::           |||   :::|||   :::   :::          :::|||
Db        376 TACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCC 435

Qy        143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162
              ::::::::::::      ||||||:::::||||||         :::|||:::||||||
Db        436 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 495

Qy        163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
              |||   ||||||           |||   ||||||::::::||||||||   ||||||
Db        496 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 552

Qy        183 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 195
              ||||||||||||||||||||||||||   ||||||:::
Db        553 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 612

Qy        195 ------------------------------------------------------------ 195

Db        613 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 672

Qy        196 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 205
                          |||:::                  :::|||   |||||||||   |||
Db        673 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 732

Qy        206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
              |||   :::      :::   ||||||||||||||   |||   ||||||
```

```
Db        733 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 789

Qy        226 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245

Db        790 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 849

Qy        246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 265

Db        850 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 909

Qy        266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285

Db        910 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 969

Qy        286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 305

Db        970 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029

Qy        306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325

Db       1030 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1086

Qy        326 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345

Db       1087 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146

Qy        346 Thr 346

Db       1147 ACC 1149

RESULT 11
US-09-171-945-124
; Sequence 124, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;  APPLICANT:  Emery, Stephen
;  APPLICANT:  Copley, Clive Graham
;  APPLICANT:  Edge, Michael Derek
;  TITLE OF INVENTION:  Monoclonal Antibody to CEA, Conjugates Comprising Said
;  TITLE OF INVENTION:  Antibody, and Their Therapeutic Use in an Adept System
;  FILE REFERENCE:  Monoclonal Antibody to CEA
;  CURRENT APPLICATION NUMBER: US/09/171,945
;  CURRENT FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  GB9703103.3
;  PRIOR FILING DATE:  1997-02-14
;  PRIOR APPLICATION NUMBER:  GB9609405.7
;  PRIOR FILING DATE:  1996-05-04
;  PRIOR APPLICATION NUMBER:  PCT/GB97/01165
;  PRIOR FILING DATE:  1997-04-29
;  NUMBER OF SEQ ID NOS:  131
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 2154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-124

Alignment Scores:
Pred. No.:              3.59e-69        Length:         2154
Score:                  623.00          Matches:        132
Percent Similarity:     53.40%          Conservative:   72
Best Local Similarity:  34.55%          Mismatches:     134
Query Match:            32.60%          Indels:         44
DB:                     3               Gaps:           7

US-09-980-881A-2 (1-360) x US-09-171-945-124 (1-2154)

Qy          3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22

Db          1 ATGTTGGCACTCTTGGTTCTGGTGACTGTGGCCCTGGCATCTGCTCATCATGGTGGTGAG 60

Qy         23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41

Db         61 CACTTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATA 120

Qy         42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61

Db        121 ATCCGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAA 180

Qy         62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81

Db        181 ATCAAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAG 240

Qy         82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101

Db        241 AATGTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTG 300

Qy        102 IleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121

Db        301 GTGGAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAG 351

Qy        122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141

Db        352 AAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCA 411

Qy        142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161

Db        412 GCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTG 471

Qy        162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181

Db        472 AAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCAT 528

Qy        182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------------------- 195

Db        529 GCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACC 588

Qy        195 ------------------------------------------------------------ 195

Db        589 TATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCT 648

Qy        196 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 204

Db        649 GTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACT 708

Qy        205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224

Db        709 CGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GAT 765

Qy        225 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 244

Db        766 GCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCT 825

Qy        245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264

Db        826 GCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCT 885

Qy        265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284

Db        886 TCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCA 945

Qy        285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304

Db        946 TATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTG 1005

Qy        305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324

Db       1006 AAAGAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACA 1062

Qy        325 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344

Db       1063 ATCTATCCTTCTGCTGGGACTTCTAAAGACTGGGCTTATGACCAAGGAATCAGATATTCC 1122

Qy        345 PheThr 346
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Db       1123 TTCACC 1128

RESULT 12
US-09-023-655-1020
; Sequence 1020, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1020:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1622 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g179933
US-09-023-655-1020

Alignment Scores:
Pred. No.:              6.17e-69      Length:         1622
Score:                  619.50        Matches:        130
Percent Similarity:     54.07%        Conservative:   76
Best Local Similarity:  34.12%        Mismatches:     128
Query Match:            32.42%        Indels:         47
DB:                     4             Gaps:           8

US-09-980-881A-2 (1-360) x US-09-023-655-1020 (1-1622)

Qy          6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla--------- 22
              :::   ::::::::::|||:::   |||                       |||
Db          1 ATGAGGCTCATCCTGCCTGTGGGTTTGATTGCTACCACTCTTGCAATTGCTCCTGTCCGC 60

Qy         23 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 42
              |||      :::|||          |||:::     :::|||      ::::::
Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         43 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62
              ::::::|||      |||   |||:::      |||   |||               :::
Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82
                          |||   |||   ||:::      :::         :::::::::
Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102
                 |||:::   :::   :::         :::|||:::   |||:::::::::   |||
Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy        103 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
              ::::::|||          :::   :::      |||   |||          |||
Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141
              :::|||::::::      :::|||   :::|||   |||   :::   :::::::::|||
Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
              :::|||:::::::::|||   |||||||||:::   |||       ||||||||||||||
Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181
              |||:::   |||::::::      :::   ||||||:::::|||||||||||||||
Db        472 AAGATT---GGGGAAAAGAATGAAAGAACAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        182 AlaArgGluTrpIleSerProAlaProCysLeuTrpPheIle------------------ 195
              ||||||||||:::|||||||||||||||   ||||||:::
Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTCCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        195 ------------------------------------------------------------ 195

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        196 ---------------GlyHis------------------AsnArgMetTrpArgLysAsn 204
                              |||:::                 ||||||||||||||||||||
Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224
              ||||||          |||:::   ||||||||||||||||||||   ||||||   :::
Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        225 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 244
                    |||                 ::::::      |||::::::   |||   |||
Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264
                 ||||||||||||   |||   |||||||||   :::|||:::|||   ::::::|||
Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 284
              :::||||||   |||||||:::   ||||||||||||||   ::::::|||||||||
Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
              ||||||                 :::||||||:::|||:::   ||||||
Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324
                    :::   |||         |||||||||   :::|||               |||
Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCACA 1062

Qy        325 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344
              :::|||         |||       ||||||   ||||||||||||||||||::::::
Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        345 Phe 345
              |||
Db       1123 TTT 1125

RESULT 13
US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
```

```
; GENERAL INFORMATION:
;  APPLICANT: Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0047-USA
;  CURRENT APPLICATION NUMBER: US/09/675,305
;  CURRENT FILING DATE:  2000-09-29
;  PRIOR APPLICATION NUMBER: US 60/156,685
;  PRIOR FILING DATE: 1999-09-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1311
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.:              4.54e-68      Length:          1311
Score:                  611.50        Matches:         141
Percent Similarity:     50.36%        Conservative:    69
Best Local Similarity:  33.81%        Mismatches:      135
Query Match:            32.00%        Indels:          72
DB:                     4             Gaps:            11

US-09-980-881A-2 (1-360) x US-09-675-305-9 (1-1311)

Qy          1 MetLysLeuCys------SerLeuAlaValLeuValProIleValLeuPheCysGluGln 18
              :::  ||||||       |||   :::|||   |||
Db         43 CTGCCTCTTTGCTGGCTCTTTTTGAAGATTCTGCAACCG------------GGGCACAGC 90

Qy         19 HisValPhe------AlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSer 36
              |||::::::       :::       :::|||:::     :::|||:::|||
Db         91 CACCTTTATAACAACCGCTATGCTGGTGATAAAGTGATAAGATTTATTCCCAAAACAGAA 150

Qy         37 ArgGlnValGlnValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnPro 56
                 :::       |||:::   ::::::       ::::::   ||||||||||||
Db        151 GAGGAAGCATATGCACTGAAGAAAATATCCTATCAACTTAAGGTGGACCTGTGGCAGCCC 210

Qy         57 ValThrAlaAspLeuIleValLys------LysLysGlnValHisPheValAsnAla 74
                 :::       :::  :::            ||||||          |||
Db        211 AGCAGTATCTCCTATGTATCAGAGGGAACAGTTACTGATGTCCATATCCCCCAAAATGGT 270

Qy         75 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyIleProCysSerValLeu 94
              |||           :::   |||   |||       :::   |||          ||||||
Db        271 TCCCGAGCC------CTGTTAGCCTTCTTACAGGAAGCCAACATCCAGTACAAGGTCCTC 324

Qy         95 LeuAlaAspValGluAspLeuIleGlnGlnGlnIleSerAsnAspThrValSerProArg 114
              :::   |||::::::      :::::::::       |||      |||         |||
Db        325 ATAGAAGATCTTCAGAAAACACTGGAGAAGGGAAGCAGCTTGCACACCCAGAGAAACCGA 384

Qy        115 AlaSerAlaSer------TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrp 132
              |||   |||       ||||||   ||||||||||||   ||||||   :::|||
Db        385 AGATCCCTCTCTGGATATAATTATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGG 444

Qy        133 IleGluPheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSer 152
              :::     :::   :::   |||       ::::::           ||||||   |||
Db        445 ATGCATCATCTGAATAAAACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCA 504

Qy        153 PheGluLysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsn 172
              :::|||         |||::::::||||||:::   ||:::            |||
Db        505 TATGAGGGAAGATCTCTTTTTATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGA 561

Qy        173 AlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeu 192
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||
Db        562 GCTGTTTGGATAGACTGTGGTATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAG 621

Qy        193 TrpPheIle---------------------------------------------------- 195
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                |||||::::
Db        622 TGGTTTGTAAAAGAAGCTCTTCTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTG 681

Qy        195 ------------------------------------------------------------ 195

Db        682 AATCATCTATATTTCTATATCATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGG 741

Qy        196 GlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGly 215
                 ::::::|||   ||||||||   ||||||      :::          |||   |||
Db        742 ACCAATGATCGATTTTGGAGAAAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGA 801

Qy        216 ThrAspLeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSer 235
                 |||   |||   |||:::      |||   ||||||:::||||||||||||
Db        802 GTGGATGCCAATAGAAACTGGAAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCAC 858

Qy        236 SerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaVal 255
                 |||   :::||||||||||||   :::||||||||||||||||||||||||||||||
Db        859 CCTTGTGATGACACATACTGTGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTA 918

Qy        256 AlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyr 275
                 |||:::|||||||||:::::::          |||:::||||||:::|||   |||:::|||
Db        919 GCTAACTTCCTTCGAAAACACAGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATAT 978

Qy        276 SerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlu 295
                 :::|||   :::::::::||||||||||||       :::       :::
Db        979 GCTCAGATGTTACTGTATCCCTATTCTTACAAATATGCAACAATTCCCAATTTTAGATGT 1038

Qy        296 LeuSerLeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArg 315
                 :::          |||   :::||||||   |||:::   ::::::            |||
Db       1039 GTGGAATCTGCAGCTTATAAAGCTGTGAATGCACTT---CAGTCAGTATACGGGGTACGA 1095

Qy        316 TyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrp 335
                 |||   :::|||       |||   |||||||||:::::   |||         ||||||
Db       1096 TACAGATATGGACCAGCCTCCACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGG 1155

Qy        336 IleTyrAspLeuGlyIleLysTyrSerPhe---------------------------- 345
                 |||      ||||||   |||:::|||
Db       1156 GCCTACAAAAATGGAATACCTTATGCATTTGCTTTCGAACTACGTGACACTGGATATTTT 1215

Qy        346 ----------------------ThrSerAsnProProValGluLysLeu 354
                                     :::|||||||||||||||:::||||||
Db       1216 GGATTTTTACTCCCAGAGATGCTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 14
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
;  APPLICANT: Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0047-USA
;  CURRENT APPLICATION NUMBER: US/10/200,344
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: US/09/675,305
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1311
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.:              4.54e-68      Length:          1311
Score:                  611.50        Matches:         141
Percent Similarity:     50.36%        Conservative:    69
```

```
Best Local Similarity:  33.81%        Mismatches:    135
Query Match:            32.00%        Indels:         72
DB:                     4             Gaps:           11

US-09-980-881A-2 (1-360) x US-10-200-344-9 (1-1311)

Qy          1 MetLysLeuCys------SerLeuAlaValLeuValProIleValLeuPheCysGluGln 18
              :::   ||||||         |||   :::|||   |||
Db         43 CTGCCTCTTTGCTGGCTCTTTTTGAAGATTCTGCAACCG------------GGGCACAGC 90

Qy         19 HisValPhe------AlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSer 36
              |||::::::         :::         :::|||:::      :::|||:::|||
Db         91 CACCTTTATAACAACCGCTATGCTGGTGATAAAGTGATAAGATTTATTCCCAAAACAGAA 150

Qy         37 ArgGlnValGlnValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnPro 56
                 :::         |||:::   ::::::         ::::::   ||||||||||||
Db        151 GAGGAAGCATATGCACTGAAGAAAATATCCTATCAACTTAAGGTGGACCTGTGGCAGCCC 210

Qy         57 ValThrAlaAspLeuIleValLys------LysLysGlnValHisPhePheValAsnAla 74
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Db        211 AGCAGTATCTCCTATGTATCAGAGGGAACAGTTACTGATGTCCATATCCCCCAAAATGGT 270

Qy         75 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyIleProCysSerValLeu 94
              |||         :::   |||   |||     :::   |||         ||||||
Db        271 TCCCGAGCC------CTGTTAGCCTTCTTACAGGAAGCCAACATCCAGTACAAGGTCCTC 324

Qy         95 LeuAlaAspValGluAspLeuIleGlnGlnGlnIleSerAsnAspThrValSerProArg 114
              :::   |||::::::      :::::::::      |||       |||         |||
Db        325 ATAGAAGATCTTCAGAAAACACTGGAGAAGGGAAGCAGCTTGCACACCCAGAGAAACCGA 384

Qy        115 AlaSerAlaSer------TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrp 132
              |||   |||         ||||||   ||||||||||||   ||||||   :::|||
Db        385 AGATCCCTCTCTGGATATAATTATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGG 444

Qy        133 IleGluPheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSer 152
              :::     :::   :::   |||     ::::::                ||||||   |||
Db        445 ATGCATCATCTGAATAAAACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCA 504

Qy        153 PheGluLysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsn 172
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Db        505 TATGAGGGAAGATCTCTTTTTATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGA 561

Qy        173 AlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeu 192
              |||:::||||||||||||||||||||||||||||||||||   ||||||||||||
Db        562 GCTGTTTGGATAGACTGTGGTATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAG 621

Qy        193 TrpPheIle---------------------------------------------------- 195
              ||||||:::
Db        622 TGGTTTGTAAAAGAAGCTCTTCTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTG 681

Qy        195 ---------------------------------------------------------- 195

Db        682 AATCATCTATATTTCTATATCATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGG 741

Qy        196 GlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGly 215
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Db        742 ACCAATGATCGATTTTGGAGAAAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGA 801

Qy        216 ThrAspLeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSer 235
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Db        802 GTGGATGCCAATAGAAACTGGAAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCAC 858

Qy        236 SerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaVal 255
                 |||   :::||||||||||||   :::||||||||||||||||||||||||||||||
Db        859 CCTTGTGATGACACATACTGTGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTA 918

Qy        256 AlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyr 275
              |||:::||||||||:::::         |||:::||||||:::|||   |||:::|||
Db        919 GCTAACTTCCTTCGAAAACACAGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATAT 978

Qy        276 SerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlu 295
              :::|||   :::::::::||||||||||||      :::      :::
Db        979 GCTCAGATGTTACTGTATCCCTATTCTTACAAATATGCAACAATTCCCAATTTTAGATGT 1038

Qy        296 LeuSerLeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArg 315
              :::         |||   :::||||||   |||:::   ::::::         |||
Db       1039 GTGGAATCTGCAGCTTATAAAGCTGTGAATGCACTT---CAGTCAGTATACGGGGTACGA 1095

Qy        316 TyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrp 335
              |||   :::|||       |||   |||||||||::::::   |||         ||||||
Db       1096 TACAGATATGGACCAGCCTCCACAACGTGTATGTGAGCTCTGGTAGCTCAATGGATTGG 1155

Qy        336 IleTyrAspLeuGlyIleLysTyrSerPhe---------------------------- 345
                 |||       ||||||   |||:::|||
Db       1156 GCCTACAAAAATGGAATACCTTATGCATTTGCTTTCGAACTACGTGACACTGGATATTTT 1215

Qy        346 ----------------------ThrSerAsnProProValGluLysLeu 354
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Db       1216 GGATTTTTACTCCCAGAGATGCTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 15
US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
;  GENERAL INFORMATION:
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Fulga, Netta
;    APPLICANT:  Mendelovitch, Simona
;    APPLICANT:  Gorecki, Marian
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/782,760
;      FILING DATE:  13-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/378,233
;      FILING DATE:  25-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/4384
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  927 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..927
US-08-782-760-5

Alignment Scores:
Pred. No.:              2.28e-67        Length:         927
Score:                  604.00          Matches:        125
Percent Similarity:     60.14%          Conservative:   44
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Best Local Similarity:  44.48%          Mismatches:    72
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US-09-980-881A-2 (1-360) x US-08-782-760-5 (1-927)

Qy        115 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 134
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Db          1 GCAAGTGGACACAGCTACACCAAGTACAACAACTGGGAAACGATTGAGGCGTGGATTCAA 60

Qy        135 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 154
                 :::          :::|||||::::::|||:::      |||||::::::||||||
Db         61 CAAGTTGCCACTGATAATCCAGACCTTGTCACTCAGAGCGTCATTGGAACCACATTTGAA 120

Qy        155 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 174
                     :::||||||||||||:::   ||||||   :::      |||   ||||||
Db        121 GGACGTAACATGTATGTCCTCAAGATT---GGTAAAACTAGACCGAATAAGCCTGCCATC 177

Qy        175 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 194
              :::||||||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTTCTCCTGCATTCTGTCAGTGGTTT 237

Qy        195 Ile---------------------------------------------------------- 195
              :::
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Qy        196 ----------------------------------GlyHis------------------ 197
                                                 |||:::
Db        298 CTGGATTTCTATGTTCTGCCTGTGGTCAACATTGATGGCTATGTCTACACCTGGACTAAG 357

Qy        198 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 217
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Db        358 GACAGAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGAC 417

Qy        218 LeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 237
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Db        418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy        238 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 257
              ||||||||||||||||      ||||||||||||   |||   ||||||:::|||
Db        475 TCTGAAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534

Qy        258 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 277
              |||:::|||   |||::::::   ||||||||||||:::::::::||||||||||||||
Db        535 TTCATCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAG 594

Qy        278 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 297
              :::::::::||||||||||||                 :::::::::|||||||||:::
Db        595 ATGATGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

Qy        298 LeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThr 317
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Qy        318 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 337
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db        712 TATGGCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTAT 771

Qy        338 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 357
              |||   ||||||||||||||||||||         |||      :::||||||   |||
Db        772 GATCAGGGAATCAAATATTCCTTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830

Qy        358 Ser 358
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Search completed: October 31, 2004, 04:39:47
Job time : 118.873 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 626.949 Seconds
(without alignments)
2944.316 Million cell updates/sec

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Perfect score: 1911
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Ygapop 10.0 , Ygapext 0.5
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Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US09980881_@CGN_1_1_811_@runat_28102004_131644_12110
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Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1849.5	96.8	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1849.5	96.8	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1832	95.9	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1808.5	94.6	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1808.5	94.6	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1729	90.5	1272	15	US-10-379-836-1	Sequence 1, Appli
7	1439.5	75.3	1037	16	US-10-115-479-63	Sequence 63, Appl
8	1393.5	72.9	1132	16	US-10-115-479-65	Sequence 65, Appl
9	889	46.5	1400	9	US-09-925-302-24	Sequence 24, Appl
10	889	46.5	1400	10	US-09-925-302-24	Sequence 24, Appl
11	623	32.6	2154	9	US-09-910-059-124	Sequence 124, App
12	621.5	32.5	1332	9	US-09-954-456-1141	Sequence 1141, Ap
13	620.5	32.5	1633	15	US-10-341-434-187	Sequence 187, App
14	620.5	32.5	1740	14	US-10-116-802-95	Sequence 95, Appl
15	619.5	32.4	1254	14	US-10-229-546-3	Sequence 3, Appli
16	619.5	32.4	1622	14	US-10-229-546-1	Sequence 1, Appli
17	619.5	32.4	1622	15	US-10-429-802-21	Sequence 21, Appl
18	619.5	32.4	1622	16	US-10-430-503-12	Sequence 12, Appl
19	619.5	32.4	1622	16	US-10-262-511-71	Sequence 71, Appl
20	619.5	32.4	1622	16	US-10-641-643-1020	Sequence 1020, Ap
21	611.5	32.0	1302	17	US-10-477-515-1	Sequence 1, Appli
22	611.5	32.0	1311	13	US-10-200-344-9	Sequence 9, Appli
23	611.5	32.0	1993	15	US-10-274-639-33	Sequence 33, Appl
24	611.5	32.0	1993	16	US-10-333-574-33	Sequence 33, Appl
25	609.5	31.9	1907	18	US-10-757-262-127	Sequence 127, App
26	591	30.9	416	9	US-09-960-352-14595	Sequence 14595, A
27	564	29.5	2128	13	US-10-200-344-13	Sequence 13, Appl
28	563	29.5	1125	9	US-09-888-615-2	Sequence 2, Appli
29	563	29.5	1332	15	US-10-176-306-75	Sequence 75, Appl
30	563	29.5	1603	15	US-10-176-306-73	Sequence 73, Appl
31	556	29.1	1826	15	US-10-252-157-453	Sequence 453, App
32	546	28.6	1200	14	US-10-200-910-7	Sequence 7, Appli
33	546	28.6	1200	18	US-10-843-130-7	Sequence 7, Appli
34	543	28.4	1870	9	US-09-910-059-112	Sequence 112, App
35	543	28.4	1870	17	US-10-608-710-3	Sequence 3, Appli
36	528.5	27.7	1050	13	US-10-200-344-11	Sequence 11, Appl
37	527.5	27.6	991	16	US-10-383-201-93	Sequence 93, Appl
38	519.5	27.2	1260	16	US-10-257-174-16	Sequence 16, Appl
39	519.5	27.2	1311	14	US-10-200-910-5	Sequence 5, Appli
40	519.5	27.2	1311	16	US-10-257-174-15	Sequence 15, Appl
41	519.5	27.2	1311	17	US-10-451-821-1	Sequence 1, Appli
42	519.5	27.2	1311	18	US-10-843-130-5	Sequence 5, Appli
43	519.5	27.2	1348	16	US-10-072-012-315	Sequence 315, App
44	519.5	27.2	1641	17	US-10-381-820A-5	Sequence 5, Appli
45	514.5	26.9	1295	17	US-10-363-829-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

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Score:                  1849.50         Matches:        355
Percent Similarity:     94.18%          Conservative:   1
Best Local Similarity:  93.92%          Mismatches:     4
Query Match:            96.78%          Indels:         18
DB:                     9               Gaps:           1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
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Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 196

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 256

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGATGTGGAAGAT 316

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 376

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
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Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 496

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
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Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 616

Qy        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 676

Qy        221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240
              ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 736

Qy        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 796

Qy        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 856

Qy        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 916

Qy        301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
              ||||||||||||||||||:::|||    ||||||||||||||||||||||||||||||||||||||||
Db        917 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 976

Qy        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGCTCAGAAACCTTATACCTAGCTCCTGCAGGTGGGGACGATTGGATCTATGATTTGGGC 1036

Qy        341 IleLysTyrSerPhe---------------------------------------------- 345
              |||||||||||||||
Db       1037 ATCAAATATTCGTTTACAATTGAACTTCCAGATACGGGCACATACGGATTCTTGCTGCCG 1096

Qy        346 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                     ||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores:
Pred. No.:              4.27e-219       Length:         1625
Score:                  1849.50         Matches:        355
Percent Similarity:     94.18%          Conservative:   1
Best Local Similarity:  93.92%          Mismatches:     4
Query Match:            96.78%          Indels:         18
DB:                     14              Gaps:           1

US-09-980-881A-2 (1-360) x US-10-212-877-1 (1-1625)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 76

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 136

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 196

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 256

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGATGTGGAAGAT 316

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 376

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 436

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 496

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
                |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        497 TTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGACTGTGGAATC 556

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATG 616

Qy        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 676

Qy        221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240
                ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 736

Qy        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 796

Qy        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 856

Qy        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 916

Qy        301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
                ||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||||
Db        917 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 976

Qy        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1036

Qy        341 IleLysTyrSerPhe---------------------------------------------- 345
                ||||||||||||||||
Db       1037 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1096

Qy        346 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1148

RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
;   LENGTH: 1728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396
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Alignment Scores:
Pred. No.:              7.12e-217       Length:         1728
Score:                  1832.00         Matches:        357
Percent Similarity:     86.27%          Conservative:   1
Best Local Similarity:  86.02%          Mismatches:     2
Query Match:            95.87%          Indels:         55
DB:                     9               Gaps:           2

US-09-980-881A-2 (1-360) x US-09-880-107-2396 (1-1728)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 79

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 139

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 199

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 259

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 319

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 379

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 439

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 499

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATC 559

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 CATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAA 619

Qy        197 ------------------------------------------------------------ 197

Db        620 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 679

Qy        198 ----------------------------------------AsnArgMetTrpArgLys 203
                                                       ||||||||||||||||
Db        680 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 739

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        740 AACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCT 799

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 859

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 CTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATC 919

Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyr 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        920 AACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATAT 979

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 TCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1039

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       1040 GTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1099

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1100 ACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATAT 1159

Qy        344 SerPhe----------------------------------------------------Th 346
              ||||||                                                    ||
Db       1160 TCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTAC 1219

Qy        346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
              |||||||||||||||||||||||||||||||||||||||||||
Db       1220 ATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1262

RESULT 4
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.:                3.93e-214      Length:          1344
Score:                    1808.50        Matches:         355
Percent Similarity:       84.76%         Conservative:    1
Best Local Similarity:    84.52%         Mismatches:      4
Query Match:              94.64%         Indels:          60
DB:                       16             Gaps:            3

US-09-980-881A-2 (1-360) x US-10-115-479-69 (1-1344)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 90

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 150

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 210

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 270

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 330

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 390

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 450

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 510

Qy        161 LeuLys----------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175
              ||||||          ||||||||||||||||||  ||||||||||||||||||
Db        511 TTAAAGGGTTTCTTTGAGCAGGTTTCTGCAAAAGAACAAGCAGCCAAAAATGCCATATGG 570

Qy        176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 630

Qy        196 GlyHis---------------------------------------------------- 197
              ||||||
Db        631 GGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTG 690

Qy        198 ----------------------------------------------------------Asn 198
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Db        691 GATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAAT 750
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```
Qy        199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 810

Qy        219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 238
              |||    ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        811 AATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 870

Qy        239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 930

Qy        259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 990

Qy        279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 1050

Qy        299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db       1051 GTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACAT 1110

Qy        319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1170

Qy        339 LeuGlyIleLysTyrSerPhe---------------------------------------- 345
              |||||||||||||||||||
Db       1171 TTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTG 1230

Qy        346 -------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                          ||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1288
```

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:

Pred. No.:	6.06e-214	Length:	1743
Score:	1808.50	Matches:	355
Percent Similarity:	84.76%	Conservative:	1
Best Local Similarity:	84.52%	Mismatches:	4
Query Match:	94.64%	Indels:	60
DB:	16	Gaps:	3

US-09-980-881A-2 (1-360) x US-10-115-479-67 (1-1743)

```
Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 79

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 139

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 199

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 259

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 319

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 379

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 439

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTT 499
```

```
Qy        161 LeuLys--------------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175
              ||||||                ||||||||||||||||||    ||||||||||||||||||
Db        500 TTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGG 559

Qy        176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 619

Qy        196 GlyHis------------------------------------------------------ 197
              ||||||
Db        620 GGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTG 679

Qy        198 ----------------------------------------------------------Asn 198
                                                                         |||
Db        680 GATTTCTATGTTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAAT 739

Qy        199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 799

Qy        219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 238
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        800 AATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 859

Qy        239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 GAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTC 919

Qy        259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 TTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCAT 979

Qy        279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 ATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTA 1039

Qy        299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db       1040 GTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACAT 1099

Qy        319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1100 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 1159

Qy        339 LeuGlyIleLysTyrSerPhe---------------------------------------- 345
              |||||||||||||||||||
Db       1160 TTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTG 1219

Qy        346 ------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                           ||||||||||||||||||||||||||||||||||||||||||||
Db       1220 CTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1277
```

RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

Alignment Scores:

Pred. No.:	2.79e-204	Length:	1272
Score:	1729.00	Matches:	338
Percent Similarity:	83.37%	Conservative:	8
Best Local Similarity:	81.45%	Mismatches:	14
Query Match:	90.48%	Indels:	55
DB:	15	Gaps:	2

US-09-980-881A-2 (1-360) x US-10-379-836-1 (1-1272)

```
Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGCTTTGCAGTCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 60

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGCGTTTCAGAGTGGCCAGGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 120

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCGGAC 180

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||   ||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        181 CTTATTGAGAAGAAAAAACAAGTCCATTTTTTTGTAAATTCATCTGATGTCGACAATGTG 240

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCCTGCTGGCAGATGTGGAAGAT 300

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 360

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||| ||||||||||||   |||||||::::::
Db        361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAACTTATAACTGAGAAGTAT 420

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||| |||||||:::||||||:::|||||||||||||
Db        421 CCTGATATGCTTACAAAAATCCACATTGGATCCTCCTATGAGAAGCACCCACTTTATGTT 480

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              ||||||||||||||||||||||||||| |||||||||:::|||||||||||||||||||
Db        481 TTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATGTGGATTGACTGTGGAATC 540

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------- 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCCAGAGAATGGATCTCCCCTGCTTCCTGCTTGTGGTTCATAGGCCATATAACTGAA 600

Qy        197 ---------------------------------------------------------- 197

Db        601 TACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATG 660

Qy        198 ----------------------------------------AsnArgMetTrpArgLys 203
                                                     ||||||||||||||||||
Db        661 CCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAG 720

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
              ||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        721 AACCGTTCTTTCTATGCGAACAATCGTTGCATCGGAACAGACCTGAACAGGAACTTTGCG 780

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        781 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGGAAACCTACTGTGGA 840

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
              ||||||||||||||||||||||   ||||||||||:::|||||||||||||||||||||
Db        841 CTTTATCCTGAGTCAGAACCAGAAGCGAAGGCGGTGGCTAATTTCTTGAGAAGAAATATC 900
```

```
Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyr 283
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACCACATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATCGTGTTTCCATAT 960

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCCTATACTCGAAGCAAAAGCAAAGACCACGAGGAATTGTCTCTAGTAGCCAGTGAAGCA 1020

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
              ||||||||||||  ||||||||||||||  ||||||||||||||  |||||||||
Db       1021 GTTCGTGCTATTCAGAAAACCAGTAAAAATATCAGGTATACACATGGCCGTGGCTCAGAA 1080

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1081 ACCTTATACCTAGCTCCTGGAGGTGCGGACGATTGGATCTATGATTTGGGCATCAAATAT 1140

Qy        344 SerPhe-------------------------------------------------------Th 346
              ||||||                                                       ||
Db       1141 TCGTTTACAATTGAACTTCGAGATACGGGCAAATACGGATTCTTGCTGCCTGAGCGTTAC 1200

Qy        346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
              ||||||||||  |||:::  ||||||||||||||||||||
Db       1201 ATCAAACCCACTTGTAAAGACGCTTTTGCCGCTGTCTCTAAAA 1243

RESULT 7
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.:              2.07e-168       Length:         1037
Score:                  1439.50         Matches:        293
Percent Similarity:     77.78%          Conservative:   1
Best Local Similarity:  77.51%          Mismatches:     2
Query Match:            75.33%          Indels:         82
DB:                     16              Gaps:           2

US-09-980-881A-2 (1-360) x US-10-115-479-63 (1-1037)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 100

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 160

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 280

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 340

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 400

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTGAGAAGTACCCACTCTATGTT 520

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              ||||||||||||||||||||  ||||||||||||||||||||
Db        521 TTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGAC--------- 571

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200

Db        571 ------------------------------------------------------------ 571

Qy        201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220

Db        571 ------------------------------------------------------------ 571

Qy        221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240
```

```
Db        571 ------------------------------------------------------------ 571

Qy        241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 ---TGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 628

Qy        261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 688

Qy        281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 748

Qy        301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
              ||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db        749 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 808

Qy        321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 868

Qy        341 IleLysTyrSerPhe---------------------------------------------- 345
              |||||||||||||||
Db        869 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 928

Qy        346 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                      ||||||||||||||||||||||||||||||||||||||||||||
Db        929 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 980

RESULT 8
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
;   LENGTH: 1132
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.:                1.27e-162      Length:          1132
Score:                    1393.50        Matches:         283
Percent Similarity:       67.38%         Conservative:    0
Best Local Similarity:    67.38%         Mismatches:      3
Query Match:              72.92%         Indels:          134
DB:                       16             Gaps:            4

US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1132)

Qy          1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ATGAAGCTTTGCAGCCTTGCAGTCCTTGTACCCATTGTTCTCTTCTGTGAGCAGCATGTC 100

Qy         21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TTCGCGTTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAA 160

Qy         41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy         61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 280

Qy         81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 AAAGCCCATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGAT 340

Qy        101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 400

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CCTGATATGCTTACAAAAATCCACATTGCATCCTCATTTGAGAAGTACCCACTCTATGTT 520

Qy        161 LeuLys---------------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175
              ||||||               ||||||||||||||||||   ||||||||||||||||||
Db        521 TTAAAGGGTTTCTTTGAGCAGGTTTCTGCAAAAGAACAAGCAGCCAAAAATGCCATATGG 580

Qy        176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        581 ATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATA 640

Qy        196 GlyHis---------------------------------------------------------- 197
              ||||||
Db        641 GGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTG 700

Qy        198 ------------------------------------------------------------Asn 198
                                                                          |||
Db        701 GATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAAT 760

Qy        199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTG 820

Qy        219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSer 238
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        821 AATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 880

Qy        239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
              ||||||||||||||||||||||||||
Db        881 GAAACCTACTGTGGACTTTATCCTGAG---------------------------------- 907

Qy        259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278

Db        907 ---------------------------------------------------------- 907

Qy        279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298

Db        907 ---------------------------------------------------------- 907

Qy        299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318

Db        907 ---------------------------------------------------------- 907

Qy        319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 ---------TCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGAT 958

Qy        339 LeuGlyIleLysTyrSerPhe---------------------------------------- 345
              |||||||||||||||||||
Db        959 TTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTG 1018

Qy        346 -------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                          ||||||||||||||||||||||||||||||||||||||||||||
Db       1019 CTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1076

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:

Pred. No.:                1.06e-99      Length:          1400
Score:                    889.00        Matches:         178
Percent Similarity:       75.21%        Conservative:    1
Best Local Similarity:    74.79%        Mismatches:      3
Query Match:              46.52%        Indels:          56
DB:                       9             Gaps:            2

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

Qy        179 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 197
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy        197 ---------------------------------------------------------- 197

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy        198 ------------------------------------------------AsnArgMetTr 201
                                                             ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189

Qy        201 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAs 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 241
              ||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        241 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        261 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        281 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 321
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        321 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        341 eLysTyrSerPhe----------------------------------------------- 345
              ||||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                   ||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 719

RESULT 10
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.:              1.06e-99        Length:         1400
Score:                  889.00          Matches:        178
Percent Similarity:     75.21%          Conservative:   1
Best Local Similarity:  74.79%          Mismatches:     3
Query Match:            46.52%          Indels:         56
DB:                     10              Gaps:           2

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

Qy        179 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 197
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy        197 ------------------------------------------------------------ 197

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy        198 ----------------------------------------------------AsnArgMetTr 201
                                                                   ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189

Qy        201 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAs 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 241
              ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        241 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        261 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        281 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 321
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        321 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        341 eLysTyrSerPhe------------------------------------------- 345
              |||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
                   ||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTGCCGCTGTCTCTAAAA 719

RESULT 11
US-09-910-059-124
; Sequence 124, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
;  APPLICANT: Copley, Clive G
;  APPLICANT:  Edge, Michael Derek
;  APPLICANT:  Emery, Stephen Charles
;  TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, a
;  TITLE OF INVENTION:  Their Therapeutic use in an Adept System
;  FILE REFERENCE: 1991-209
;  CURRENT APPLICATION NUMBER: US/09/910,059
;  CURRENT FILING DATE:  2001-07-23
;  PRIOR APPLICATION NUMBER: US 09/171,945
;  PRIOR FILING DATE: 1998-10-29
;  PRIOR APPLICATION NUMBER: PCT/GB97/01165
;  PRIOR FILING DATE: 1997-04-29
;  PRIOR APPLICATION NUMBER: GB 9703103.3
;  PRIOR FILING DATE: 1997-02-14
;  PRIOR APPLICATION NUMBER: GB9609405.7
;  PRIOR FILING DATE: 1996-05-04
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 2154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: humanised pre-pro HCPB-linker-Fd sequence
US-09-910-059-124

Alignment Scores:
Pred. No.:              2.7e-66         Length:         2154
Score:                  623.00          Matches:        132
Percent Similarity:     53.40%          Conservative:   72
Best Local Similarity:  34.55%          Mismatches:     134
Query Match:            32.60%          Indels:         44
DB:                     9               Gaps:           7

US-09-980-881A-2 (1-360) x US-09-910-059-124 (1-2154)

Qy          3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
              :::   :::|||   |||||||||  :::  |||          |||
Db          1 ATGTTGGCACTCTTGGTTCTGGTGACTGTGGCCCTGGCATCTGCTCATCATGGTGGTGAG 60

Qy         23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41
                 |||:::     :::|||                        :::   :::
Db         61 CACTTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATA 120

Qy         42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61
              ::::::   |||   :::|||  :::|||      |||:::|||   :::
Db        121 ATCCGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAA 180

Qy         62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81
              |||             |||   |||   |||   |||   |||         |||:::
Db        181 ATCAAACCTCACAGTACAGTTGACTTCCCTGTTAAAGCAGAAGATACTGTCACTGTGGAG 240

Qy         82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
                 |||     :::   :::       |||||:::::::::::::   ::::::
Db        241 AATGTTCTAAAGCAGAATGAACTACAATATCAAGGTACTGATAAGCAACCTGAGAAATGTG 300

Qy        102 IleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
              ::::::   |||      :::                |||||:::         ||||||
Db        301 GTGGAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAG 351

Qy        122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141
              :::|||:::             |||  :::|||  :::  :::         :::|||
Db        352 AAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCA 411

Qy        142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
              :::::::::::      ||||||::::::||||||      :::|||:::|||
Db        412 GCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTG 471

Qy        162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181
              ||||||   ||||||            |||   ||||||::::::|||||||||   |||
Db        472 AAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCAT 528

Qy        182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----------------- 195
```

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Db        529 GCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACC 588

Qy        195 ------------------------------------------------------------ 195

Db        589 TATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCT 648

Qy        196 ---------------GlyHis-----------------AsnArgMetTrpArgLysAsn 204

Db        649 GTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACT 708

Qy        205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224

Db        709 CGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GAT 765

Qy        225 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 244

Db        766 GCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCT 825

Qy        245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264

Db        826 GCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCT 885

Qy        265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 284

Db        886 TCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCA 945

Qy        285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304

Db        946 TATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTG 1005

Qy        305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324

Db       1006 AAAGAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACA 1062

Qy        325 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344

Db       1063 ATCTATCCTTCTGCTGGGACTTCTAAAGACTGGGCTTATGACCAAGGAATCAGATATTCC 1122

Qy        345 PheThr 346

Db       1123 TTCACC 1128

RESULT 12
US-09-954-456-1141
; Sequence 1141, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1141
;   LENGTH: 1332
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1141

Alignment Scores:
Pred. No.:                1.86e-66        Length:          1332
Score:                    621.50          Matches:         134
Percent Similarity:       53.66%          Conservative:    71
Best Local Similarity:    35.08%          Mismatches:      132
Query Match:              32.52%          Indels:          45
DB:                       9               Gaps:            8

US-09-980-881A-2 (1-360) x US-09-954-456-1141 (1-1332)

Qy          3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22

Db         24 ATGTTGGCACTCTTGGTTCTGGTGACTGTGGCCCTGGCATCTGCTCATCATGGTGGTGAG 83

Qy         23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41

Db         84 CACTTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATA 143

Qy         42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61

Db        144 ATCCGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAA 203

Qy         62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81

Db        204 ATCAAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAG 263

Qy         82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101

Db        264 AATGTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTG 323

Qy        102 IleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121

Db        324 GTGGAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAG 374

Qy        122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141

Db        375 AAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCA 434

Qy        142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161

Db        435 GCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTG 494

Qy        162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181

Db        495 AAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCAT 551

Qy        182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----------------- 195

Db        552 GCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACC 611

Qy        195 ------------------------------------------------------------ 195

Db        612 TATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCT 671

Qy        196 ---------------GlyHis-----------------AsnArgMetTrpArgLysAsn 204

Db        672 GTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACT 731

Qy        205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224

Db        732 CGCTCCACCCATACTGGATCT---AGCATTGGCACAGACCCCAACAGAAATTTT---GAT 785

Qy        225 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 244
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Db        786 GCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCT 845

Qy        245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264

Db        846 GCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCT 905

Qy        265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 284

Db        906 TCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCA 965

Qy        285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304

Db        966 TATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTG 1025

Qy        305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324

Db       1026 AAAGAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACA 1082

Qy        325 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344

Db       1083 ATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCC 1142

Qy        345 PheThr 346

Db       1143 TTCACC 1148

RESULT 13
US-10-341-434-187
; Sequence 187, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
;  FILE REFERENCE: 9U 204 205 R1
;  CURRENT APPLICATION NUMBER: US/10/341,434
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 60/348,164
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: US 60/348,119
;  PRIOR FILING DATE: 2002-01-15
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 187
;   LENGTH: 1633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (12)..(1262)
;   OTHER INFORMATION:
US-10-341-434-187

Alignment Scores:
Pred. No.:              3.48e-66        Length:         1633
Score:                  620.50          Matches:        130
Percent Similarity:     54.19%          Conservative:   77
Best Local Similarity:  34.03%          Mismatches:     128
Query Match:            32.47%          Indels:         47
DB:                     15              Gaps:           8

US-09-980-881A-2 (1-360) x US-10-341-434-187 (1633)

Qy          5 SerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla------ 22

Db          9 ACCATGAGGCTCATCCTGCCTGTGGGTTTGATTGCTACCACTCTTGCAATTGCTCCTGTC 68

Qy         23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41

Db         69 CGCTTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATC 128

Qy         42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61

Db        129 ATAAAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCAC 188

Qy         62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81

Db        189 GTAGCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAG 248

Qy         82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101

Db        249 TCTGCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAG 308

Qy        102 IleGlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120

Db        309 ATTGAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TAC 359

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

Db        360 GCAAAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTAT 419

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

Db        420 CCTGAAATGGTCTCTCGTATTAAAATTGCATCTACTGTTGAAGATAATCCACTATATGTT 479

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

Db        480 CTGAAGATT---GGGGAAAAGAATGAAACAAGAAAGGCTATTTTTATGGATTGTGGCATT 536

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle--------------- 195

Db        537 CACGCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAA 596

Qy        195 ------------------------------------------------------------ 195

Db        597 ACTTATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTT 656

Qy        196 ------------------GlyHis------------------AsnArgMetTrpArgLys 203

Db        657 CCTGTGTTCAATGTTGATGGATATATTTCGTCATGGACAAAGAACCGCATGTGGAGAAAA 716

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223

Db        717 AATCGTTCCAAGAACCAAAACTCCAAATCCATCGGCACTGACCTCAACAGGAATTTT--- 773

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243

Db        774 AATGCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGC 833

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263

Db        834 TCTGCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTG 893

Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyr 283

Db        894 AATGAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTAT 953

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303

Db        954 GGATATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGC 1013

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323

Db       1014 ACTGATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCA 1070

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343

Db       1071 ACAATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACAC 1130

Qy        344 SerPhe 345

Db       1131 ACATTT 1136

RESULT 14
US-10-116-802-95
; Sequence 95, Application US/10116802
; Publication No. US20030065157A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Amy Lasek
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0045 US
;  CURRENT APPLICATION NUMBER: US/10/116,802
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: 60/281,593
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 519
;  SOFTWARE: PERL Program
; SEQ ID NO 95
;   LENGTH: 1740
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1656674CB1
US-10-116-802-95

Alignment Scores:
Pred. No.:              3.87e-66      Length:          1740
Score:                  620.50        Matches:         130
Percent Similarity:     54.19%        Conservative:    77
Best Local Similarity:  34.03%        Mismatches:      128
Query Match:            32.47%        Indels:          47
DB:                     14            Gaps:            8

US-09-980-881A-2 (1-360) x US-10-116-802-95 (1-1740)

Qy          5 SerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla------ 22
              ::::::   ::::::::::|||:::   |||                    |||
Db          3 ACCATGAGGCTCATCCTGCCTGTGGGTTTGATTGCTACCACTCTTGCAATTGCTCCTGTC 62

Qy         23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41
                 |||         :::|||           |||:::     :::|||      :::
Db         63 CGCTTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATC 122

Qy         42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61
              :::::::::|||      |||   |||:::      |||   |||
Db        123 ATAAAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCAC 182

Qy         62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81
              :::                |||   |||   |||:::      :::         ::::::
Db        183 GTAGCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAG 242

Qy         82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
              :::   |||:::   :::   :::         :::|||:::   |||:::::::::
Db        243 TCTGCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAG 302

Qy        102 IleGlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
              |||::::::|||          :::   :::      |||   |||         |||
Db        303 ATTGAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TAC 353

Qy        121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
                 :::|||::::::      :::|||   :::|||   |||   :::   :::::::::
Db        354 GCAAAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTAT 413

Qy        141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
              |||:::|||:::::::::|||   |||||||||:::   |||      ||||||||||
Db        414 CCTGAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTT 473

Qy        161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
              |||||||:::   |||::::::      :::   ||||||::::::||||||||||
Db        474 CTGAAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATT 530

Qy        181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle--------------- 195
              ||||||||||||||:::|||||||||||||||   ||||||:::
Db        531 CACGCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAA 590

Qy        195 ------------------------------------------------------------ 195

Db        591 ACTTATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTT 650

Qy        196 -----------------GlyHis-----------------AsnArgMetTrpArgLys 203
                              |||:::                |||||||||||||||||
Db        651 CCTGTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAA 710

Qy        204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
              |||||||||          |||:::   ||||||||||||||||||||   ||||||
Db        711 AATCGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT--- 767

Qy        224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
              :::      |||           ::::::     |||::::::    |||   |||
Db        768 AATGCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGC 827

Qy        244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
                    ||||||||||||   |||   |||||||||   :::|||:::|||   ::::::
Db        828 TCTGCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTG 887

Qy        264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
              |||:::||||||   ||||||:::   ||||||||||||||   ::::::|||||||||
Db        888 AATGAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTAT 947

Qy        284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
                    ||||||          :::||||||:::|||:::   ||||||
Db        948 GGATATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGC 1007

Qy        304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
                        :::      |||          |||||||||   :::|||
Db       1008 ACTGATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCA 1064

Qy        324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
              |||:::|||          |||          ||||||   |||||||||||||||||:::
Db       1065 ACAATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACAC 1124

Qy        344 SerPhe 345
              :::|||
Db       1125 ACATTT 1130

RESULT 15
US-10-229-546-3
; Sequence 3, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
;  APPLICANT: Weich, Nadine S.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREFOR
;  FILE REFERENCE: MPI01-156P1RNM
;  CURRENT APPLICATION NUMBER: US/10/229,546
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: 60/316,575
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1254
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1254)
US-10-229-546-3

Alignment Scores:
Pred. No.:              2.99e-66      Length:          1254
Score:                  619.50        Matches:         130
Percent Similarity:     54.07%        Conservative:    76
Best Local Similarity:  34.12%        Mismatches:      128
Query Match:            32.42%        Indels:          47
DB:                     14            Gaps:            8

US-09-980-881A-2 (1-360) x US-10-229-546-3 (1-1254)

Qy          6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla--------- 22
```

```
Db          1 ATGAGGCTCATCCTGCCTGTGGGTTTGATTGCTACCACTCTTGCAATTGCTCCTGTCCGC 60

Qy         23 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 42

Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         43 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62

Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82

Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102

Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy        103 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121

Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141

Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161

Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181

Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------------ 195

Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        195 ---------------------------------------------------------- 195

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        196 ---------------GlyHis------------------AsnArgMetTrpArgLysAsn 204

Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224

Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        225 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 244

Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264

Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284

Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304

Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324

Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

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Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        345 Phe 345

Db       1123 TTT 1125
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Search completed: October 31, 2004, 08:40:28
Job time : 640.949 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:34:50 ; Search time 25.7797 Seconds
(without alignments)
869.503 Million cell updates/sec

Title: US-09-980-881A-3
Perfect score: 1798
Sequence: 1 FQSGQVLAALPRTSRQVQVL.....IKYSFTSNPPVEKLLPLSLK 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1717	95.5	386	4	US-09-813-133A-2	Sequence 2, Appli
2	1699.5	94.5	423	1	US-07-649-591B-3	Sequence 3, Appli
3	1699.5	94.5	423	1	US-08-277-540-3	Sequence 3, Appli
4	1699.5	94.5	423	1	US-08-430-787A-3	Sequence 3, Appli
5	1699.5	94.5	423	2	US-08-869-057-2	Sequence 2, Appli
6	1688.5	93.9	423	4	US-09-813-133A-4	Sequence 4, Appli
7	646.5	36.0	404	1	US-08-696-139-2	Sequence 2, Appli
8	637.5	35.5	415	2	US-08-860-882A-57	Sequence 57, Appl
9	637.5	35.5	415	4	US-09-011-769A-39	Sequence 39, Appl
10	637.5	35.5	424	4	US-09-011-769A-56	Sequence 56, Appl
11	632	35.2	417	1	US-07-649-591B-7	Sequence 7, Appli
12	632	35.2	417	1	US-08-277-540-7	Sequence 7, Appli
13	632	35.2	417	1	US-08-430-787A-7	Sequence 7, Appli
14	622	34.6	417	1	US-07-649-591B-6	Sequence 6, Appli
15	622	34.6	417	1	US-08-277-540-6	Sequence 6, Appli
16	622	34.6	417	1	US-08-430-787A-6	Sequence 6, Appli
17	622	34.6	417	4	US-09-917-254-66	Sequence 66, Appl
18	619.5	34.5	716	3	US-09-171-945-125	Sequence 125, App
19	612	34.0	437	4	US-09-675-305-10	Sequence 10, Appl
20	612	34.0	437	4	US-10-200-344-10	Sequence 10, Appl
21	610	33.9	307	2	US-08-782-760-6	Sequence 6, Appli
22	610	33.9	307	5	PCT-US96-00995-6	Sequence 6, Appli
23	609.5	33.9	396	1	US-07-649-591B-4	Sequence 4, Appli
24	609.5	33.9	396	1	US-08-277-540-4	Sequence 4, Appli
25	609.5	33.9	396	1	US-08-430-787A-4	Sequence 4, Appli
26	582	32.4	306	1	US-08-696-139-4	Sequence 4, Appli
27	567	31.5	329	4	US-09-011-769A-51	Sequence 51, Appl
28	567	31.5	349	4	US-09-011-769A-47	Sequence 47, Appl
29	560	31.1	349	4	US-09-011-769A-60	Sequence 60, Appl
30	559	31.1	349	4	US-09-011-769A-64	Sequence 64, Appl
31	554	30.8	399	4	US-09-710-099-8	Sequence 8, Appli
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33	549.5	30.6	417	1	US-07-649-591B-8	Sequence 8, Appli
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35	549.5	30.6	417	1	US-08-430-787A-8	Sequence 8, Appli
36	549	30.5	613	3	US-09-171-945-113	Sequence 113, App
37	534.5	29.7	350	4	US-09-675-305-12	Sequence 12, Appl
38	534.5	29.7	350	4	US-10-200-344-12	Sequence 12, Appl
39	532.5	29.6	419	1	US-07-649-591B-5	Sequence 5, Appli
40	532.5	29.6	419	1	US-08-277-540-5	Sequence 5, Appli
41	532.5	29.6	419	1	US-08-430-787A-5	Sequence 5, Appli
42	527.5	29.3	436	4	US-09-710-099-6	Sequence 6, Appli
43	527.5	29.3	436	4	US-10-200-910-6	Sequence 6, Appli
44	516.5	28.7	417	3	US-08-640-906-4	Sequence 4, Appli
45	516.5	28.7	417	3	US-09-395-936-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 95.5%; Score 1717; DB 4; Length 386;
Best Local Similarity 99.4%; Pred. No. 8.3e-181;
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
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Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
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Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFT 324
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Db        323 ETLYLAPGGGDDWIYDLGIKYSFT 346
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RESULT 2

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US-07-649-591B-3
; Sequence 3, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-3

  Query Match             94.5%;  Score 1699.5;  DB 1;  Length 423;
  Best Local Similarity   89.8%;  Pred. No. 8.2e-179;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db  '      23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
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Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

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Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
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Db        263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
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Db        323 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
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Db        383 T 383
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RESULT 3
US-08-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-3

  Query Match             94.5%;  Score 1699.5;  DB 1;  Length 423;
  Best Local Similarity   89.8%;  Pred. No. 8.2e-179;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
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Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy        176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
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Db        203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
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Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
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Db        323 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
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Db        383 T 383


RESULT 4
US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-3

  Query Match             94.5%;  Score 1699.5;  DB 1;  Length 423;
  Best Local Similarity   89.8%;  Pred. No. 8.2e-179;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
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Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy        176 -------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
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Db        203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
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Db        263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
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Db        323 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
              |
Db        383 T 383


RESULT 5
US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Plasma
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23..401
US-08-869-057-2

  Query Match             94.5%;  Score 1699.5;  DB 2;  Length 423;
  Best Local Similarity   89.8%;  Pred. No. 8.2e-179;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82
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```
Qy          61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy         121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy         176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                            ||||||||||||||||||||||||||||
Db         203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy         204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy         264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         323 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy         324 T 324
               |
Db         383 T 383
```

RESULT 6
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match 93.9%; Score 1688.5; DB 4; Length 423;
Best Local Similarity 89.2%; Pred. No. 1.4e-177;
Matches 322; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

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Qy           1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy          61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy         121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy         176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                            ||||||||||||||||||||||||||||
Db         203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy         204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy         264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         323 TRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy         324 T 324
               |
Db         383 T 383
```

RESULT 7
US-08-696-139-2
; Sequence 2, Application US/08696139
; Patent No. 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hershberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Sterner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-696-139-2

Query Match 36.0%; Score 646.5; DB 1; Length 404;
Best Local Similarity 38.0%; Pred. No. 1.8e-62;
Matches 137; Conservative 60; Mismatches 121; Indels 43; Gaps 6;

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Qy           1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
               |:  :|          : :|  | :| :|  |:| :   |     | | | | |:  |:
Db          10 FEGEKVFRVNVEDENDISLLHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVED 69

Qy          61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
                 |  : :   ||: ::  ::: |  :     | :   ||:|::   | :| : :|  :||
Db          70 FLEQNELQYEVLINNLRSVLEAQFDSRV---RTTGHSYEKYNNWETIEAWTKQVTSENPD 126

Qy         121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 173
               ::::  ||::|    :|:||| ||    | ||::||| ||||||| ||| ||:
Db         127 LISRTAIGTTFLGNNIYLLKV-GKPGPNKPAIFMDCGFHAREWISHAFCQWFVREAVLTY 185

Qy         174 ----------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                    |:      |||||| ||  |   ||||| ||||
Db         186 GYESHMTEFLNKLDFYVLPVLNIDGYIYTWTKNRMWRKTRSTNAGTTCIGTDPNRNF-DA 244
```

```
Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||  |||:  | |||||   ||| | ||:| |:| |:: ||||:::||||| |::|||| 
Db        245 GWCTTGASTDPCDETYCGSAAESEKETKALADFIRNNLSSIKAYLTIHSYSQMILYPYSY 304

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
                  ::: ||: :|  ||: :  |   |:||:| |: |:| | || ||| || ||||||
Db        305 DYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGATTIYPAAGGSDDWAYDQGIKYSF 363

Qy        324 T 324
              |
Db        364 T 364
```

RESULT 8
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM,JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-882A-57

Query Match 35.5%; Score 637.5; DB 2; Length 415;
Best Local Similarity 36.0%; Pred. No. 1.8e-61;
Matches 130; Conservative 68; Mismatches 120; Indels 43; Gaps 6;

```
Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |:  :|         : ::: | :| :|  |:| :   |      | | | | |   |: 
Db         20 FEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKPHSTVDFRVKAEDTVTVEN 79

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               |  : :   ||:::: :::: |  :     ||:   ||:|:    | :| : :   :|
```

```
Db         80 VLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYNKWETIEAWTQQVATENPA 136

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 173
              ::::  ||::||   :|:||| ||    | ||::||| |||||||||| ||:
Db        137 LISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHAREWISPAFCQWFVREAVRTY 195

Qy        174 ----------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                     |:      :| ||| || :  : ||||| ||||
Db        196 GREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRSTHTGSSCIGTDPNRNF-DA 254

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||| ||| : | |||||   ||| | ||:| |:|  :: ||||:::||||| :::|||| 
Db        255 GWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIKAYLTIHSYSQMMIYPYSY 314

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
                  ::: ||: :|   |: :  :   |:||:| |: |:| | || ||| || ||:|||
Db        315 AYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYPAAGGSDDWAYDQGIRYSF 373

Qy        324 T 324
              |
Db        374 T 374
```

RESULT 9
US-09-011-769A-39
; Sequence 39, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39

Query Match 35.5%; Score 637.5; DB 4; Length 415;

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  Best Local Similarity   36.0%;  Pred. No. 1.8e-61;
  Matches  130;  Conservative   68;  Mismatches  120;  Indels   43;  Gaps    6;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |:  :|          : ::: | :| :|  |:| :   |      | | | | |   |:
Db         20 FEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKPHSTVDFRVKAEDTVTVEN 79

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              |  : :   ||:::: :::: |  :     ||:   ||:|:    | :| : :   :|
Db         80 VLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYNKWETIEAWTQQVATENPA 136

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 173
              ::::  ||::||   :|:||| ||    | ||::||| |||||||||| ||:
Db        137 LISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHAREWISPAFCQWFVREAVRTY 195

Qy        174 ----------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                   |:      :| ||| || :  : ||||| ||||
Db        196 GREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRSTHTGSSCIGTDPNRNF-DA 254

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||| ||| : | |||||   ||| | ||:| |:|  :: ||||:::|||||  :::||||
Db        255 GWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIKAYLTIHSYSQMMIYPYSY 314

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
                ::: ||: :|   |: :  :   |:||:| |: |:| | || ||| || ||:|||
Db        315 AYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYPAAGGSDDWAYDQGIRYSF 373

Qy        324 T 324
              |
Db        374 T 374


RESULT 10
US-09-011-769A-56
; Sequence 56, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 56:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 424 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-56

  Query Match             35.5%;  Score 637.5;  DB 4;  Length 424;
  Best Local Similarity   36.0%;  Pred. No. 1.9e-61;
  Matches  130;  Conservative   68;  Mismatches  120;  Indels   43;  Gaps    6;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |:  :|          : ::: | :| :|  |:| :   |      | | | | |   |:
Db         29 FEGEKVFRVNVEDENHINIIRELASTTQIDFWKPDSVTQIKPHSTVDFRVKAEDTVTVEN 88

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              |  : :   ||:::: :::: |  :     ||:   ||:|:    | :| : :   :|
Db         89 VLKQNELQYKVLISNLRNVVEAQFDSRV---RATGHSYEKYNKWETIEAWTQQVATENPA 145

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 173
              ::::  ||::||   :|:||| ||    | ||::||| |||||||||| ||:
Db        146 LISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHAREWISPAFCQWFVREAVRTY 204

Qy        174 ----------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                   |:      :| ||| || :  : ||||| ||||
Db        205 GREIQVTELLDKLDFYVLPVLNIDGYIYTWTKSRFWRKTRSTHTGSSCIGTDPNRNF-DA 263

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||| ||| : | |||||   ||| | ||:| |:|  :: ||||:::|||||  :::||||
Db        264 GWCEIGASRNPCDETYCGPAAESEKETKALADFIRNKLSSIKAYLTIHSYSQMMIYPYSY 323

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
                ::: ||: :|   |: :  :   |:||:| |: |:| | || ||| || ||:|||
Db        324 AYKLGENNAELNALAKATVKEL-ASLHGTKYTYGPGATTIYPAAGGSDDWAYDQGIRYSF 382

Qy        324 T 324
              |
Db        383 T 383


RESULT 11
US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
```

```
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-7

  Query Match            35.2%;  Score 632;  DB 1;  Length 417;
  Best Local Similarity  38.2%;  Pred. No. 7.4e-61;
  Matches  138;  Conservative   57;  Mismatches  122;  Indels   44;  Gaps    7;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |   :|     :  :   ||:||| : |:  | |      |      | | |:  :   :::
Db         21 FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVNMTVDFRVSEKESQTIQS 80

Qy         61 HLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYHSLNEIYSWIEFITERHP 119
               |    |   :|: |::: |::|    | :: | |   | :|:  ::| || | : |:||
Db         81 TLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYNDWDKIVSWTEKMLEKHP 137

Qy        120 DMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------ 173
              :|:::| |||: |  ||||||: ||:   : ||::|||||||||||||| ||:
Db        138 EMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHAREWISPAFCQWFVYQATKS 196

Qy        174 -GHN-----------------------------RMWRKNRSFYANNHCIGTDLNRNFAS 202
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Db        197 YGKNKIMTKLLDRMNFYVLPVFNVDGYIWSWTQDRMWRKNRSRNQNSTCIGTDLNRNF-D 255

Qy        203 KHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYS 262
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Db        316 YTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYKTSGSSLDWVYDLGIKHT 374

Qy        323 F 323
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Db        375 F 375


RESULT 12
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-7

  Query Match            35.2%;  Score 632;  DB 1;  Length 417;
  Best Local Similarity  38.2%;  Pred. No. 7.4e-61;
  Matches  138;  Conservative   57;  Mismatches  122;  Indels   44;  Gaps    7;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |   :|     :  :   ||:||| : |:  | |      |      | | |:  :   :::
Db         21 FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVNMTVDFRVSEKESQTIQS 80

Qy         61 HLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYHSLNEIYSWIEFITERHP 119
               |    |   :|: |::: |::|    | :: | |   | :|:  ::| || | : |:||
Db         81 TLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYNDWDKIVSWTEKMLEKHP 137

Qy        120 DMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------ 173
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Db        138 EMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHAREWISPAFCQWFVYQATKS 196

Qy        174 -GHN-----------------------------RMWRKNRSFYANNHCIGTDLNRNFAS 202
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Qy        203 KHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYS 262
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Db        256 VSWDSSPNTNKPCLNVYRGPAPESEKETKAVTNFIRSHLNSIKAYITFHSYSQMLLIPYG 315

Qy        263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYS 322
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Db        316 YTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYKTSGSSLDWVYDLGIKHT 374

Qy        323 F 323
              |
Db        375 F 375


RESULT 13
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-7

  Query Match             35.2%;  Score 632;  DB 1;  Length 417;
  Best Local Similarity   38.2%;  Pred. No. 7.4e-61;
  Matches  138;  Conservative   57;  Mismatches  122;  Indels   44;  Gaps    7;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |   :|     :  :   ||:||| : |:  | |      |     | | |:  :   :::
Db         21 FDREKVFRVKLQNEKHASVLKNLTQSIELDFWYPDAIHDIAVNMTVDFRVSEKESQTIQS 80

Qy         61 HLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYHSLNEIYSWIEFITERHP 119
              |    |   :|: |::: |::|    | :: | |   | :|:  ::| || | : |:||
Db         81 TLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYNDWDKIVSWTEKMLEKHP 137

Qy        120 DMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------ 173
              :|:::| |||: |  ||||||: ||:   : ||::|||||||||||||| ||:
Db        138 EMVSRIKIGSTVEDNPLYVLKI-GKKDGERKAIFMDCGIHAREWISPAFCQWFVYQATKS 196

Qy        174 -GHN-----------------------------RMWRKNRSFYANNHCIGTDLNRNFAS 202
               | |                             ||||||||   |: ||||||||||
Db        197 YGKNKIMTKLLDRMNFYVLPVFNVDGYIWSWTQDRMWRKNRSRNQNSTCIGTDLNRNF-D 255

Qy        203 KHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYS 262
              |      ::  |   | |  |||| | ||| :|:| ::| ||||||: ||||| :: ||
Db        256 VSWDSSPNTNKPCLNVYRGPAPESEKETKAVTNFIRSHLNSIKAYITFHSYSQMLLIPYG 315

Qy        263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYS 322
              ||     :|::|  ||  |  |:  |   ||| :|  : |:|   |   ||:||||||::
Db        316 YTFKLPPNHQDLLKVARIATDAL-STRYETRYIYGPIASTIYKTSGSSLDWVYDLGIKHT 374

Qy        323 F 323
              |
Db        375 F 375


RESULT 14
US-07-649-591B-6
; Sequence 6, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-6

  Query Match             34.6%;  Score 622;  DB 1;  Length 417;
  Best Local Similarity   35.5%;  Pred. No. 9.4e-60;
  Matches  128;  Conservative   71;  Mismatches  118;  Indels   44;  Gaps    7;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         21 FDREKVFRVKPQDEKQADIIKDLAKTNELDFWYPGATHHVAANMMVDFRVSEKESQAIQS 80

Qy         61 HLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYHSLNEIYSWIEFITERHP 119
              |: : :   :|: |::: |::|    : :  | |   | :|::  :| :| | : :::|
Db         81 ALDQNKMHYEILIHDLQEEIEKQFDVKEDIPGRHS---YAKYNNWEKIVAWTEKMMDKYP 137

Qy        120 DMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------ 173
              :|:::| |||: |  ||||||: |::   : ||::|||||||||:||||| ||:
Db        138 EMVSRIKIGSTVEDNPLYVLKI-GEKNEERKAIFMDCGIHAREWVSPAFCQWFVYQATKT 196

Qy        174 -------------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFAS 202
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Db        197 YGRNKIMTKLLDRMNFYILPVFNVDGYIWSWTKNRMWRKNRSKNQNSKCIGTDLNRNF-N 255

Qy        203 KHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYS 262
              |      ::  |:: | |  |||| | ||| :|:| ::|:|| ||: ||||| ::|||
Db        256 ASWNSIPNTNDPCADNYRGSAPESEKETKAVTNFIRSHLNEIKVYITFHSYSQMLLFPYG 315

Qy        263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYS 322
              ||     :||:|: ||      :  |   ||| :|    |:|   |   || ||||||::
Db        316 YTSKLPPNHEDLAKVAKIGTDVL-STRYETRYIYGPIESTIYPISGSSLDWAYDLGIKHT 374

Qy        323 F 323
              |
Db        375 F 375


RESULT 15
US-08-277-540-6
; Sequence 6, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
```

```
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  417 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-6

  Query Match             34.6%;  Score 622;  DB 1;  Length 417;
  Best Local Similarity   35.5%;  Pred. No. 9.4e-60;
  Matches  128;  Conservative   71;  Mismatches  118;  Indels   44;  Gaps    7;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         21 FDREKVFRVKPQDEKQADIIKDLAKTNELDFWYPGATHHVAANMMVDFRVSEKESQAIQS 80

Qy         61 HLNVSGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYYEQYHSLNEIYSWIEFITERHP 119
               |: : :   :|: |::: |::|    : :  | |   | :|::  :| :| | : :::|
Db         81 ALDQNKMHYEILIHDLQEEIEKQFDVKEDIPGRHS---YAKYNNWEKIVAWTEKMMDKYP 137

Qy        120 DMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------ 173
              :|:::| |||: |  ||||||: |::   : ||::|||||||||:||||| ||:
Db        138 EMVSRIKIGSTVEDNPLYVLKI-GEKNERRKAIFMDCGIHAREWVSPAFCQWFVYQATKT 196

Qy        174 -------------------------GH------NRMWRKNRSFYANNHCIGTDLNRNFAS 202
                                        |:      |||||||||   |: ||||||||||  :
Db        197 YGRNKIMTKLLDRMNFYILPVFNVDGYIWSWTKNRMWRKNRSKNQNSKCIGTDLNRNF-N 255

Qy        203 KHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYS 262
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Db        256 ASWNSIPNTNDPCADNYRGSAPESEKETKAVTNFIRSHLNEIKVYITFHSYSQMLLFPYG 315

Qy        263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYS 322
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Db        316 YTSKLPPNHEDLAKVAKIGTDVL-STRYETRYIYGPIESTIYPISGSSLDWAYDLGIKHT 374

Qy        323 F 323
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Db        375 F 375


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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 1798
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1717	95.5	386	14	US-10-212-877-2	Sequence 2, Appli
3	1699.5	94.5	423	14	US-10-379-836-17	Sequence 17, Appl
4	1688.5	93.9	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1688.5	93.9	423	14	US-10-212-877-4	Sequence 4, Appli
6	1676	93.2	428	15	US-10-115-479-68	Sequence 68, Appl
7	1676	93.2	428	15	US-10-115-479-70	Sequence 70, Appl
8	1615.5	89.8	423	14	US-10-379-836-2	Sequence 2, Appli
9	1487.5	82.7	422	14	US-10-379-836-18	Sequence 18, Appl
10	1466.5	81.6	422	14	US-10-379-836-16	Sequence 16, Appl
11	1297	72.1	322	15	US-10-115-479-64	Sequence 64, Appl
12	1258	70.0	354	15	US-10-115-479-66	Sequence 66, Appl
13	816.5	45.4	211	9	US-09-925-302-467	Sequence 467, App
14	816.5	45.4	211	10	US-09-925-302-467	Sequence 467, App
15	646.5	36.0	416	15	US-10-074-978A-269	Sequence 269, App
16	637.5	35.5	402	14	US-10-379-836-20	Sequence 20, Appl
17	637.5	35.5	417	15	US-10-074-978A-267	Sequence 267, App
18	637.5	35.5	417	15	US-10-074-978A-268	Sequence 268, App
19	637.5	35.5	417	16	US-10-477-515-3	Sequence 3, Appli
20	630.5	35.1	416	15	US-10-074-978A-270	Sequence 270, App
21	622	34.6	417	14	US-10-229-546-2	Sequence 2, Appli
22	622	34.6	417	14	US-10-229-546-9	Sequence 9, Appli
23	622	34.6	417	14	US-10-341-434-188	Sequence 188, App
24	622	34.6	417	15	US-10-262-511-72	Sequence 72, Appl
25	619.5	34.5	716	9	US-09-910-059-125	Sequence 125, App
26	618	34.4	416	15	US-10-074-978A-266	Sequence 266, App
27	612	34.0	434	16	US-10-477-515-2	Sequence 2, Appli
28	612	34.0	437	13	US-10-200-344-10	Sequence 10, Appl
29	612	34.0	437	14	US-10-274-639-12	Sequence 12, Appl
30	612	34.0	437	15	US-10-333-574-12	Sequence 12, Appl
31	610	33.9	437	17	US-10-757-262-128	Sequence 128, App
32	569	31.6	374	9	US-09-888-615-61	Sequence 61, Appl
33	569	31.6	444	14	US-10-176-306-74	Sequence 74, Appl
34	554	30.8	399	14	US-10-200-910-8	Sequence 8, Appli
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37	549	30.5	613	16	US-10-608-710-4	Sequence 4, Appli
38	536.5	29.8	419	15	US-10-072-012-788	Sequence 788, App
39	534.5	29.7	350	13	US-10-200-344-12	Sequence 12, Appl
40	530	29.5	286	15	US-10-072-012-887	Sequence 887, App
41	527.5	29.3	419	15	US-10-257-174-40	Sequence 40, Appl
42	527.5	29.3	436	14	US-10-200-910-6	Sequence 6, Appli
43	527.5	29.3	436	15	US-10-072-012-316	Sequence 316, App
44	527.5	29.3	436	15	US-10-072-012-784	Sequence 784, App
45	527.5	29.3	436	15	US-10-257-174-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 95.5%; Score 1717; DB 9; Length 386;
Best Local Similarity 99.4%; Pred. No. 7.9e-162;
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202
```

```
Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFT 324
              |||||||||||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 2
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-212-877-2

  Query Match             95.5%;  Score 1717;  DB 14;  Length 386;
  Best Local Similarity   99.4%;  Pred. No. 7.9e-162;
  Matches  322;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFT 324
              |||||||||||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-836-17

  Query Match             94.5%;  Score 1699.5;  DB 14;  Length 423;
  Best Local Similarity   89.8%;  Pred. No. 5e-160;
  Matches  324;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy        176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                           ||||||||||||||||||||||||||||
Db        203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
              |
Db        383 T 383


RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

  Query Match             93.9%;  Score 1688.5;  DB 9;  Length 423;
  Best Local Similarity   89.2%;  Pred. No. 6.2e-159;
  Matches  322;  Conservative    0;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82
```

```
Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy        176 ---------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                                  ||||||||||||||||||||||||||
Db        203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        323 TRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
              |
Db        383 T 383
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RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Query Match 93.9%; Score 1688.5; DB 14; Length 423;
Best Local Similarity 89.2%; Pred. No. 6.2e-159;
Matches 322; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

```
Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHITQFY 202

Qy        176 ---------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                                  ||||||||||||||||||||||||||
Db        203 GIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        323 TRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 382

Qy        324 T 324
              |
Db        383 T 383
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RESULT 6
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match 93.2%; Score 1676; DB 15; Length 428;
Best Local Similarity 88.0%; Pred. No. 1.1e-157;

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  Matches  322;  Conservative    0;  Mismatches    2;  Indels   42;  Gaps    2;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH 175
              ||||||||||||||||||||     |||||| ||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGH 202

Qy        176 ------------------------------------NRMWRKNRSFYANNHCIGTDLNR 198
                                                   ||||||||||||||||||||||
Db        203 ITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNR 262

Qy        199 NFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIV 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 NFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIV 322

Qy        259 FPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLG 318
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        323 FPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLG 382

Qy        319 IKYSFT 324
              ||||||
Db        383 IKYSFT 388


RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-70

  Query Match             93.2%;  Score 1676;  DB 15;  Length 428;
  Best Local Similarity   88.0%;  Pred. No. 1.1e-157;
  Matches  322;  Conservative    0;  Mismatches    2;  Indels   42;  Gaps    2;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH 175
              ||||||||||||||||||||     |||||| ||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGH 202

Qy        176 ------------------------------------NRMWRKNRSFYANNHCIGTDLNR 198
                                                   ||||||||||||||||||||||
Db        203 ITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNR 262

Qy        199 NFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIV 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 NFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIV 322

Qy        259 FPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLG 318
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        323 FPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLG 382

Qy        319 IKYSFT 324
              ||||||
Db        383 IKYSFT 388


RESULT 8
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 423
;   TYPE: PRT
```

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;   ORGANISM: Papio hamadryas
US-10-379-836-2

  Query Match            89.8%;  Score 1615.5;  DB 14;  Length 423;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-151;
  Matches  307;  Conservative    8;  Mismatches    9;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |||||||||||||||||||||||||||||||||||||||||| |||||||||:||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIEKKKQVHFFVNSSDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||::||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIELITEKYPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              ||||||||||:||:||||||||||||||||:||||||||||||||||||||||
Db        143 MLTKIHIGSSYEKHPLYVLKVSGKEQTAKNAMWIDCGIHAREWISPAFCLWFIGHITEYY 202

Qy        176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                           ||||||||||||| |||||||||||||
Db        203 GIIGEYTNLLRHVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNRCIGTDLNRNFASK 262

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||||||| |||||||||||||||| ||||:||||||| ||||||||||||||||||||
Db        263 HWCEEGASSFSCSETYCGLYPESEPEAKAVANFLRRNINHIKAYISMHSYSQHIVFPYSY 322

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              ||||||||||||||||||||||:||||| |||| |||||||||||| ||||||||||||
Db        323 TRSKSKDHEELSLVASEAVRAIQKTSKNIRYTHGRGSETLYLAPGGADDWIYDLGIKYSF 382

Qy        324 T 324
              |
Db        383 T 383


RESULT 9
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-379-836-18

  Query Match            82.7%;  Score 1487.5;  DB 14;  Length 422;
  Best Local Similarity   78.1%;  Pred. No. 6.1e-139;
  Matches  282;  Conservative   20;  Mismatches   22;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |||||||:||||||||:||||||||:||||||: | |||:||||||||||:|||
Db         22 FQSGQVLSALPRTSRQVQLLQNLTTTYEVVLWQPVTAEFIEKKKEVHFFVNASDVDSVKA 81

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              |||||  || :||: :|||||:||  |||||||||||||||||||||||| |||:|||
Db         82 HLNVSRIPFNVLMNNVEDLIEQQTFNDTVSPRASASYYEQYHSLNEIYSWIEVITEQHPD 141

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              || ||:||||||||||||||||  |||||||||||||||||||||:
Db        142 MLQKIYIGSSFEKYPLYVLKVSGKEQRIKNAIWIDCGIHAREWISPAFCLWFIGYVTQFH 201

Qy        176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                           ||||||||| : || |:||||||||||
Db        202 GKENLYTRLLRHVDFYIMPVMNVDGYDYTWKKNRMWRKNRSAHKNNRCVGTDLNRNFASK 261

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||:||||||||||||||||||||||||| ||||||: |||||||||||| |:|||||
Db        262 HWCEKGASSSSCSETYCGLYPESEPEVKAVADFLRRNIDHIKAYISMHSYSQQILFPYSY 321

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              |||||||||||||||||||  :|||||||| |||:||||||| ||||||||||||
Db        322 NRSKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSESLYLAPGGSDDWIYDLGIKYSF 381

Qy        324 T 324
              |
Db        382 T 382


RESULT 10
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-379-836-16

  Query Match            81.6%;  Score 1466.5;  DB 14;  Length 422;
  Best Local Similarity   76.7%;  Pred. No. 7.5e-137;
  Matches  277;  Conservative   22;  Mismatches   25;  Indels   37;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              |||| ||:|||||||||:|||||||||:|||||||: | |||:||||||||::|||
Db         22 FQSGHVLSALPRTSRQVQLLQNLTTTYEVVLWQPVTAEFIEKKKEVHFFVNASDVNSVKA 81

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              :|| | || :||: :|||||||| |||||||||:|||||||||||||||| |||:|||
Db         82 YLNASRIPFNVLMNNVEDLIQQQTSNDTVSPRASSSYYEQYHSLNEIYSWIEVITEQHPD 141

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH----- 175
              || ||:||||:|||||||||||   |||||||||||||||||||||||:
Db        142 MLQKIYIGSSYEKYPLYVLKVSGKEHRVKNAIWIDCGIHAREWISPAFCLWFIGYVTQFH 201

Qy        176 ------------------------------NRMWRKNRSFYANNHCIGTDLNRNFASK 203
                                           ||||||||| : || |:||||||||||
Db        202 GKENTYTRLLRHVDFYIMPVMNVDGYDYTWKKNRMWRKNRSVHMNNRCVGTDLNRNFASK 261

Qy        204 HWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSY 263
              ||||:|||| |||||||||||||||||| ||||||| |||||||||||| |:|||||
Db        262 HWCEKGASSFSCSETYCGLYPESEPEVKAVADFLRRNINHIKAYISMHSYSQQILFPYSY 321

Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
              |||||||||||||||||||  :|||||||| |||:||||||| ||||||||||||
Db        322 NRSKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSESLYLAPGGSDDWIYDLGIKYSF 381

Qy        324 T 324
              |
Db        382 T 382


RESULT 11
US-10-115-479-64
```

```
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-64

  Query Match             72.1%;  Score 1297;  DB 15;  Length 322;
  Best Local Similarity   79.6%;  Pred. No. 3.7e-120;
  Matches  258;  Conservative    0;  Mismatches    2;  Indels   64;  Gaps    1;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
              |||||||||||||||||||||||||| ||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWID------------------------- 177

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEECASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                                                  ||||||||||||||||||||
Db        178 -------------------------------------CGLYPESEPEVKAVASFLRRN 198

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        199 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGS 258

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFT 324
              ||||||||||||||||||||||||
Db        259 ETLYLAPGGGDDWIYDLGIKYSFT 282


RESULT 12
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
```

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;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-66

  Query Match            70.0%;  Score 1258;  DB 15;  Length 354;
  Best Local Similarity  68.0%;  Pred. No. 3.2e-116;
  Matches  249;  Conservative    0;  Mismatches    1;  Indels  116;  Gaps    3;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLK-----VSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGH 175
              |||||||||||||||||||     |||||| ||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGH 202

Qy        176 ------------------------------------NRMWRKNRSFYANNHCIGTDLNR 198
                                                 |||||||||||||||||||||||
Db        203 ITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKKNRMWRKNRSFYANNHCIGTDLNR 262

Qy        199 NFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIV 258
              ||||||||||||||||||||||||||
Db        263 NFASKHWCEEGASSSSCSETYCGLYPE------------------------------- 289

Qy        259 FPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLG 318
                                                  ||||||||||||||||||||
Db        290 ----------------------------------------SETLYLAPGGGDDWIYDLG 308

Qy        319 IKYSFT 324
              ||||||
Db        309 IKYSFT 314


RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

  Query Match            45.4%;  Score 816.5;  DB 9;  Length 211;
  Best Local Similarity  90.6%;  Pred. No. 1.3e-72;
  Matches  154;  Conservative    1;  Mismatches    6;  Indels    9;  Gaps    2;

Qy        163 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 214
              |||   | | :         ||||||||||||||||||||||||||||||||||||||
Db          3 WIS-MLCRWLMWMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 61

Qy        215 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        275 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

  Query Match            45.4%;  Score 816.5;  DB 10;  Length 211;
  Best Local Similarity  90.6%;  Pred. No. 1.3e-72;
  Matches  154;  Conservative    1;  Mismatches    6;  Indels    9;  Gaps    2;

Qy        163 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 214
              |||   | | :         ||||||||||||||||||||||||||||||||||||||
Db          3 WIS-MLCRWLMWMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 61

Qy        215 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        275 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
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;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-10-074-978A-269

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Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFI------- 173
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Qy        264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSF 323
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Qy        324 T 324
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Db        376 T 376


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Job time : 78.339 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:35:31 ; Search time 312.936 Seconds
(without alignments)
1196.740 Million cell updates/sec

Title: US-09-980-881A-3
Perfect score: 1798
Sequence: 1 FQSGQVLAALPRTSRQVQVL.....IKYSFTSNPPVEKLLPLSLK 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1798	100.0	338	25	US-09-980-881-3	Sequence 3, Appli
2	1798	100.0	338	25	US-09-980-881A-3	Sequence 3, Appli
3	1786	99.3	360	27	US-10-170-205E-13306	Sequence 13306, A
4	1786	99.3	360	34	US-10-803-180-126	Sequence 126, App
5	1786	99.3	360	35	US-10-918-754-1941	Sequence 1941, Ap
6	1786	99.3	360	36	US-60-452-680-21530	Sequence 21530, A
7	1786	99.3	360	36	US-60-453-050-13037	Sequence 13037, A
8	1786	99.3	360	36	US-60-453-135-13037	Sequence 13037, A
9	1786	99.3	360	36	US-60-455-444-6989	Sequence 6989, Ap
10	1786	99.3	360	36	US-60-465-241-6989	Sequence 6989, Ap
11	1786	99.3	360	36	US-60-466-412-13037	Sequence 13037, A
12	1786	99.3	360	36	US-60-495-114-1941	Sequence 1941, Ap
13	1786	99.3	366	24	US-09-949-003C-3190	Sequence 3190, Ap
14	1786	99.3	366	24	US-09-949-003C-3191	Sequence 3191, Ap
15	1785	99.3	360	25	US-09-980-881-2	Sequence 2, Appli
16	1785	99.3	360	25	US-09-980-881A-2	Sequence 2, Appli
17	1784	99.2	360	22	US-09-791-537-142876	Sequence 142876,
18	1784	99.2	360	24	US-09-949-003C-2616	Sequence 2616, Ap
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20	1717	95.5	386	1	PCT-US02-08289-2	Sequence 2, Appli
21	1717	95.5	386	28	US-10-212-877-2	Sequence 2, Appli
22	1699.5	94.5	423	1	PCT-US03-26773-2	Sequence 2, Appli
23	1699.5	94.5	423	3	US-07-959-944A-3	Sequence 3, Appli
24	1699.5	94.5	423	22	US-09-791-537-96834	Sequence 96834, A
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27	1699.5	94.5	423	30	US-10-486-034-2	Sequence 2, Appli
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30	1694.5	94.2	423	27	US-10-170-205E-13305	Sequence 13305, A
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34	1694.5	94.2	423	36	US-60-453-050-13036	Sequence 13036, A
35	1694.5	94.2	423	36	US-60-453-135-13036	Sequence 13036, A
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37	1694.5	94.2	423	36	US-60-465-241-6988	Sequence 6988, Ap
38	1694.5	94.2	423	36	US-60-466-412-13036	Sequence 13036, A
39	1694.5	94.2	423	36	US-60-495-114-1942	Sequence 1942, Ap
40	1694.5	94.2	424	22	US-09-760-475-1824	Sequence 1824, Ap
41	1694.5	94.2	424	28	US-10-227-425-1824	Sequence 1824, Ap
42	1694.5	94.2	429	24	US-09-949-003C-3188	Sequence 3188, Ap
43	1694.5	94.2	429	24	US-09-949-003C-3189	Sequence 3189, Ap
44	1688.5	93.9	423	1	PCT-US02-08289-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-09-980-881-3
; Sequence 3, Application US/09980881
; GENERAL INFORMATION:
; APPLICANT: AKIRA MATSUMOTO
; TITLE OF INVENTION: Human Brain Carboxypeptidase B
; FILE REFERENCE: MAT-101PCT
; CURRENT APPLICATION NUMBER: US/09/980,881
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: JP 1999-125169
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-980-881-3

Query Match 100.0%; Score 1798; DB 25; Length 338;

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RESULT 2
US-09-980-881A-3
; Sequence 3, Application US/09980881A
; GENERAL INFORMATION:
;  APPLICANT: AKIRA MATSUMOTO
;  TITLE OF INVENTION: Human Brain Carboxypeptidase B
;  FILE REFERENCE: MAT-101PCT
;  CURRENT APPLICATION NUMBER: US/09/980,881A
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: JP   1999-125169
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-980-881A-3

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RESULT 3
US-10-170-205E-13306
; Sequence 13306, Application US/10170205E
; GENERAL INFORMATION:
;  APPLICANT: ADAMS, Mark
;  TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
;  TITLE OF INVENTION:  CAPTURE AGENTS, AND USES THEREOF
;  FILE REFERENCE: CL001381
;  CURRENT APPLICATION NUMBER: US/10/170,205E
;  CURRENT FILING DATE:  2002-06-13
;  NUMBER OF SEQ ID NOS: 40312
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13306
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-170-205E-13306

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RESULT 4
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; Sequence 126, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-803-180-126

  Query Match             99.3%;  Score 1786;  DB 34;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         143 MLTKIHIGSSPEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy         181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy         241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy         301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
                ||||||||||||||||||||| ||||||||||||||||
Db         323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 5
US-10-918-754-1941
; Sequence 1941, Application US/10918754
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001480
;  CURRENT APPLICATION NUMBER: US/10/918,754
;  CURRENT FILING DATE:  2004-08-16
;  NUMBER OF SEQ ID NOS: 91238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1941
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-918-754-1941

  Query Match             99.3%;  Score 1786;  DB 35;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
                ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSPEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
                ||||||||||||||||||||| ||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 6
US-60-452-680-21530
; Sequence 21530, Application US/60452680
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  GRUPE, Andrew
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001450
;  CURRENT APPLICATION NUMBER: US/60/452,680
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 116213
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21530
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-452-680-21530

  Query Match             99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
                ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSPEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
                ||||||||||||||||||||| ||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 7
US-60-453-050-13037
; Sequence 13037, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-050-13037

  Query Match             99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82
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Qy          61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy         121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy         181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy         241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy         301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
               |||||||||||||||||||| ||||||||||||||||
Db         323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 8
US-60-453-135-13037
; Sequence 13037, Application US/60453135
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-135-13037

  Query Match             99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
               |||||||||||||||||||| ||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 9
US-60-455-444-6989
; Sequence 6989, Application US/60455444
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  BEGOVICH, Ann
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001455
;  CURRENT APPLICATION NUMBER: US/60/455,444
;  CURRENT FILING DATE:  2003-03-18
;  NUMBER OF SEQ ID NOS: 50986
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-455-444-6989

  Query Match             99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
               |||||||||||||||||||| ||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 10
US-60-465-241-6989
; Sequence 6989, Application US/60465241
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  BEGOVICH, Ann
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001468
;  CURRENT APPLICATION NUMBER: US/60/465,241
;  CURRENT FILING DATE:  2003-04-23
;  NUMBER OF SEQ ID NOS: 258418
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-465-241-6989

  Query Match             99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy         121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
                    |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy         181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy         241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy         301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
                    |||||||||||||||||||| ||||||||||||||||
Db         323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 11
US-60-466-412-13037
; Sequence 13037, Application US/60466412
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001466
;  CURRENT APPLICATION NUMBER: US/60/466,412
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 429241
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-466-412-13037

  Query Match           99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
                ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
                ||||||||||||||||||||| ||||||||||||||||
Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 12
US-60-495-114-1941
; Sequence 1941, Application US/60495114
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001480
;  CURRENT APPLICATION NUMBER: US/60/495,114
;  CURRENT FILING DATE:  2003-08-15
;  NUMBER OF SEQ ID NOS: 91238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1941
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-495-114-1941

  Query Match           99.3%;  Score 1786;  DB 36;  Length 360;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
                ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
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Db        323 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360


RESULT 13
US-09-949-003C-3190
; Sequence 3190, Application US/09949003C
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
;  TITLE OF INVENTION:  DISORDERS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000791
;  CURRENT APPLICATION NUMBER: US/09/949,003C
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,446
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 74065
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3190
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-949-003C-3190

  Query Match           99.3%;  Score 1786;  DB 24;  Length 366;
  Best Local Similarity   99.4%;  Pred. No. 9.4e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         29 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 88

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
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Db        149 MLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 208

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
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Db        209 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 268

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
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Db        269 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 328

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
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Db        329 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 366


RESULT 14
US-09-949-003C-3191
; Sequence 3191, Application US/09949003C
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
;  TITLE OF INVENTION:  DISORDERS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000791
;  CURRENT APPLICATION NUMBER: US/09/949,003C
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,446
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 74065
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3191
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-949-003C-3191

  Query Match           99.3%;  Score 1786;  DB 24;  Length 366;
  Best Local Similarity   99.4%;  Pred. No. 9.4e-181;
  Matches  336;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         29 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 88

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
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Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
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Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
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Db        329 ETLYLAPGGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 366


RESULT 15
US-09-980-881-2
; Sequence 2, Application US/09980881
; GENERAL INFORMATION:
;  APPLICANT: AKIRA MATSUMOTO
;  TITLE OF INVENTION: Human Brain Carboxypeptidase B
;  FILE REFERENCE: MAT-101PCT
;  CURRENT APPLICATION NUMBER: US/09/980,881
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: JP   1999-125169
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-980-881-2

  Query Match           99.3%;  Score 1785;  DB 25;  Length 360;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-180;
  Matches  335;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 60
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Db         23 FQSGQVLAALPRTSRQVQVLQNLTTTYEIVLWQPVTADLIVKKKQVHFFVNASDVDNVKA 82

Qy         61 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 120
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Db         83 HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYYEQYHSLNEIYSWIEFITERHPD 142

Qy        121 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 180
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Db        143 MLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCGIHAREWISPAFCLWFIGHNRMWR 202

Qy        181 KNRSFYANNHCIGTDLNRNFASKHWCEECASSSSCSETYCGLYPESEPEVKAVASFLRRN 240
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Db        203 KNRSFYANNHCIGTDLNSNFVSKHWCEECASSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy        241 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
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Db        263 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGS 322

Qy        301 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338
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Db        323 ETLYLAPGGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360


Search completed: October 28, 2004, 20:01:44
Job time : 313.936 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 03:40:54 ; Search time 98.464 Seconds
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2439.944 Million cell updates/sec

Title: US-09-980-881A-3
Perfect score: 1798
Sequence: 1 FQSGQVLAALPRTSRQVQVL.....IKYSFTSNPPVEKLLPLSLK 338

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Ygapop 10.0 , Ygapext 0.5
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1749.5	97.3	1625	4	US-09-813-133A-1	Sequence 1, Appli
2	1732	96.3	1272	2	US-08-869-057-1	Sequence 1, Appli
3	1732	96.3	1749	1	US-07-649-591B-2	Sequence 2, Appli
4	1732	96.3	1749	1	US-08-277-540-2	Sequence 2, Appli
5	1732	96.3	1749	1	US-08-430-787A-2	Sequence 2, Appli
6	646.5	36.0	1215	1	US-08-696-139-1	Sequence 1, Appli
7	637.5	35.5	1263	2	US-08-860-882A-56	Sequence 56, Appl
8	637.5	35.5	1263	4	US-09-011-769A-38	Sequence 38, Appl
9	637.5	35.5	1284	2	US-08-860-882A-71	Sequence 71, Appl
10	637.5	35.5	1284	4	US-09-011-769A-55	Sequence 55, Appl
11	622	34.6	1622	4	US-09-023-655-1020	Sequence 1020, Ap
12	619.5	34.5	1311	4	US-09-675-305-9	Sequence 9, Appli
13	619.5	34.5	1311	4	US-10-200-344-9	Sequence 9, Appli
14	619.5	34.5	2154	3	US-09-171-945-124	Sequence 124, App
15	610	33.9	927	2	US-08-782-760-5	Sequence 5, Appli
16	610	33.9	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	582	32.4	921	1	US-08-696-139-3	Sequence 3, Appli
18	571.5	31.8	2128	4	US-09-675-305-13	Sequence 13, Appl
19	571.5	31.8	2128	4	US-10-200-344-13	Sequence 13, Appl
20	567	31.5	999	2	US-08-860-882A-67	Sequence 67, Appl
21	567	31.5	999	4	US-09-011-769A-50	Sequence 50, Appl
22	567	31.5	1053	2	US-08-860-882A-64	Sequence 64, Appl
23	567	31.5	1053	4	US-09-011-769A-46	Sequence 46, Appl
24	560	31.1	1053	4	US-09-463-451-27	Sequence 27, Appl
c 25	560	31.1	1053	4	US-09-463-451-28	Sequence 28, Appl
26	560	31.1	1059	2	US-08-860-882A-74	Sequence 74, Appl
27	560	31.1	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	559	31.1	1059	2	US-08-860-882A-77	Sequence 77, Appl
29	559	31.1	1059	4	US-09-011-769A-63	Sequence 63, Appl
30	554	30.8	1200	4	US-09-710-099-7	Sequence 7, Appli
31	554	30.8	1200	4	US-10-200-910-7	Sequence 7, Appli
32	549	30.5	1870	3	US-09-171-945-112	Sequence 112, App
33	534.5	29.7	1050	4	US-09-675-305-11	Sequence 11, Appl
34	534.5	29.7	1050	4	US-10-200-344-11	Sequence 11, Appl
35	527.5	29.3	1311	4	US-09-710-099-5	Sequence 5, Appli
36	527.5	29.3	1311	4	US-10-200-910-5	Sequence 5, Appli
37	516.5	28.7	1251	3	US-08-640-906-3	Sequence 3, Appli
38	516.5	28.7	1251	3	US-09-395-936-3	Sequence 3, Appli
39	491.5	27.3	1257	3	US-08-640-906-1	Sequence 1, Appli
40	491.5	27.3	1257	3	US-09-395-936-1	Sequence 1, Appli
41	467.5	26.0	945	4	US-09-710-099-3	Sequence 3, Appli
42	467.5	26.0	945	4	US-09-710-099-11	Sequence 11, Appl
43	467.5	26.0	945	4	US-10-200-910-3	Sequence 3, Appli
44	467.5	26.0	945	4	US-10-200-910-11	Sequence 11, Appl
45	465.5	25.9	2247	4	US-09-710-099-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

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Best Local Similarity:	94.38%	Mismatches:	2
Query Match:	97.30%	Indels:	18
DB:	4	Gaps:	1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 83 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

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Db        143 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 202

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
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Db        203 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 262

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
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Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
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Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
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Db        383 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 442

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
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Db        443 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 502

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              |||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db        503 GTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCC 562

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180
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Db        563 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGA 622

Qy        181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200
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Db        683 GCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGT 742

Qy        221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 240
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Qy        261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280
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Qy        281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300
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Db       1103 TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1148

RESULT 2
US-08-869-057-1
; Sequence 1, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    PUBLICATION INFORMATION:
;      AUTHORS:  Eaton, Dan L.
;      AUTHORS:  Malloy, Beth E.
;      AUTHORS:  Tsai, Siao P
;      AUTHORS:  Henzel, William
;      AUTHORS:  Drayna, Dennis
;      TITLE:  Isolation, Molecular Cloning, and Partial
;      TITLE:  Characterization of a No. 5985562el Carboxypeptidase B
;      TITLE:  from Human Plasma
;      JOURNAL:  J. Biol. Chem.
;      VOLUME:  266
;      ISSUE:  32
;      PAGES:  21833-21838
;      DATE:  No. 5985562 15-1991
US-08-869-057-1

Alignment Scores:
Pred. No.:                3.8e-213        Length:          1272
Score:                    1732.00         Matches:         338
Percent Similarity:       86.01%          Conservative:    0
Best Local Similarity:    86.01%          Mismatches:      0
Query Match:              96.33%          Indels:          55
DB:                       2               Gaps:            2

US-09-980-881A-3 (1-338) x US-08-869-057-1 (1-1272)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
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Db         67 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 126

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 186

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 246

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
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Db        247 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 306

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
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Db        307 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 366

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 426

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 486

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
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Db        487 GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCC 546

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis---------------- 175
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Db        547 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTAT 606

Qy        175 ------------------------------------------------------------ 175

Db        607 GGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 666

Qy        176 -----------------------------------AsnArgMetTrpArgLysAsnArg 183
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Db        667 GTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGT 726

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
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Db        727 TCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAA 786

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT 846

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
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Db        847 CCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAG 906

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
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Db        907 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTAT 966

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
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Db        967 ACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1026

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
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Db       1027 GCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1086

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 TACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1146

Qy        324 ------------------------------------------------------ThrSerAs 326
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Db       1147 ACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAA 1206

Qy        326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
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RESULT 3
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  hybridization probe
;      LOCATION:  133 to 178
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  potential clip site
;      LOCATION:  380 to 382
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  signal sequence
;      LOCATION:  41 to 106
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-07-649-591B-2

Alignment Scores:
Pred. No.:                6.58e-213       Length:          1749
Score:                    1732.00         Matches:         338
Percent Similarity:       86.01%          Conservative:    0
Best Local Similarity:    86.01%          Mismatches:      0
Query Match:              96.33%          Indels:          55
DB:                       1               Gaps:            2

US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 286
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Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
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Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db        347 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db        407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 466

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db        467 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 526

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db        527 GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCC 586

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------------- 175
Db        587 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTAT 646

Qy        175 ------------------------------------------------------------ 175
Db        647 GGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706

Qy        176 ----------------------------------AsnArgMetTrpArgLysAsnArg 183
Db        707 GTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGT 766

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db        767 TCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAA 826

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db        827 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT 886

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db        887 CCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAG 946

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
Db        947 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTAT 1006

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db       1007 ACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1066

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db       1067 GCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1126

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db       1127 TACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1186

Qy        324 ----------------------------------------------------ThrSerAs 326
Db       1187 ACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAA 1246

Qy        326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
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RESULT 4
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-277-540-2

Alignment Scores:
Pred. No.:              6.58e-213      Length:          1749
Score:                  1732.00        Matches:         338
Percent Similarity:     86.01%         Conservative:    0
Best Local Similarity:  86.01%         Mismatches:      0
Query Match:            96.33%         Indels:          55
DB:                     1              Gaps:            2

US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db        107 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db        167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db        227 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 286

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db        287 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 346

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db        347 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406
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Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
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Db        407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 466

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
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Db        467 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 526

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
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Db        527 GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCC 586

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------------- 175
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Db        587 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTAT 646

Qy        175 ------------------------------------------------------------ 175

Db        647 GGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706

Qy        176 ----------------------------------AsnArgMetTrpArgLysAsnArg 183
                                                 ||||||||||||||||||||||
Db        707 GTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGT 766

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
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Db        767 TCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAA 826

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
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Db        827 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT 886

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
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Db        887 CCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAG 946

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
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Db        947 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTAT 1006

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
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Db       1007 ACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1066

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
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Db       1067 GCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1126

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
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Db       1127 TACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1186

Qy        324 ------------------------------------------------------ThrSerAs 326
                                                                     ||||||||
Db       1187 ACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAA 1246

Qy        326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
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Db       1247 CCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283

RESULT 5
US-08-430-787A-2
; Sequence 2, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-787A-2

Alignment Scores:
Pred. No.:              6.58e-213       Length:         1749
Score:                  1732.00         Matches:        338
Percent Similarity:     86.01%          Conservative:   0
Best Local Similarity:  86.01%          Mismatches:     0
Query Match:            96.33%          Indels:         55
DB:                     1               Gaps:           2

US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
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Db        227 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 286

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 346

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 466
```

```
Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 526

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCC 586

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--------------- 175
              |||||||||||||||||||||||||||||||||||||||||||
Db        587 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTAT 646

Qy        175 ------------------------------------------------------------ 175

Db        647 GGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706

Qy        176 -----------------------------------AsnArgMetTrpArgLysAsnArg 183
                                                  |||||||||||||||||||||||
Db        707 GTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGT 766

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 TCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAA 826

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT 886

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        887 CCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAG 946

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTAT 1006

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 ACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1066

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 GCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1126

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 TACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1186

Qy        324 ------------------------------------------------------ThrSerAs 326
                                                                     ||||||||
Db       1187 ACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAA 1246

Qy        326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
              |||||||||||||||||||||||||||||||||||
Db       1247 CCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1283
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```
RESULT 6
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1215 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1215
US-08-696-139-1

Alignment Scores:
Pred. No.:                4.55e-73        Length:          1215
Score:                    646.50          Matches:         137
Percent Similarity:       54.57%          Conservative:    60
Best Local Similarity:    37.95%          Mismatches:      121
Query Match:              35.96%          Indels:          43
DB:                       1               Gaps:            6

US-09-980-881A-3 (1-338) x US-08-696-139-1 (1-1215)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||:::      :::|||                                 :::   :::|||
Db         28 TTCGAAGGGGAGAAGGTGTTCCGTGTCAATGTTGAAGATGAAAATGACATCAGCTTACTC 87

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
                 |||   :::|||   :::|||       |||:::|||   :::         |||
Db         88 CATGAGTTGGCCAGCACCAGGCAGATTGACTTCTGGAAACCAGATTCTGTCACACAAATC 147

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                           |||   |||   |||   |||   |||:::      |||:::
Db        148 AAACCTCACAGTACAGTTGACTTCCGTGTGAAAGCAGAAGATATTTTGGCTGTGGAAGAC 207

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
               |||      :::   :::         ||||||:::   ::::::      ::::::
Db        208 TTTCTGGAGCAGAATGAACTACAATATGAGGTACTCATAAACAACCTGAGATCTGTGCTC 267

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              :::   |||    :::              |||   :::         ||||||:::
Db        268 GAGGCTCAGTTTGACAGCAGAGTC---------CGTACAACTGGACACAGTTATGAGAAG 318

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              |||::::::          |||   :::|||   :::   :::|||       :::||||||
Db        319 TACAACAACTGGGAAACGATCGAGGCTTCGACTAAGCAAGTCACCAGTGAAAATCCAGAC 378

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ::::::::::::      ||||||:::::|||           :::|||:::||||||
Db        379 CTCATCTCTCGCACAGCCATCGGAACTACATTTTTAGGAAACAATATATACCTCCTCAAG 438
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Qy       141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db       439 GTT---GGCAAACCTGGACCAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 495

Qy       161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 173
Db       496 AGAGAATGGATTTCCCATGCATTTTGCCAGTGGTTTGTGAGAGAGGCTGTTCTCACCTAT 555

Qy       173 ---------- 173
Db       556 GGATATGAGAGTCACATGACAGAATTCCTCAACAAGCTAGACTTTTATGTCTTGCCTGTG 615

Qy       174 ----------GlyHis----------AsnArgMetTrpArgLysAsnArg 183
Db       616 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGAAAGACCCGC 675

Qy       184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db       676 TCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 732

Qy       204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db       733 GGGTGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGCT 792

Qy       224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db       793 GCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAACCTCTCCTCC 852

Qy       244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
Db       853 ATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCTTATTCCTAT 912

Qy       264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db       913 GATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCTGCCGTGAAA 972

Qy       284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db       973 GAACTT---GCTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCTACAACAATC 1029

Qy       304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db      1030 TATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAATATTCCTTC 1089

Qy       324 Thr 324
Db      1090 ACC 1092
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```
RESULT 7
US-08-860-882A-56
; Sequence 56, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1263 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-56

Alignment Scores:
Pred. No.:                7.07e-72      Length:          1263
Score:                    637.50        Matches:         130
Percent Similarity:       54.85%        Conservative:    68
Best Local Similarity:    36.01%        Mismatches:      120
Query Match:              35.46%        Indels:          43
DB:                       2             Gaps:            6

US-09-980-881A-3 (1-338) x US-08-860-882A-56 (1-1263)

Qy         1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db        58 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 117

Qy        21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db       118 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 177

Qy        41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db       178 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 237

Qy        61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db       238 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 297

Qy        81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db       298 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 348

Qy       101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db       349 TACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCC 408

Qy       121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db       409 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 468

Qy       141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db       469 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 525

Qy       161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 173
Db       526 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 585

Qy       173 ---------- 173
Db       586 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 645
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Qy        174 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 183
                          |||:::                  :::|||   |||||||||   |||
Db        646 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 705

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
              |||   :::      :::   ||||||||||||||||   ||||||||||||
Db        706 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 762

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
              |||||||||   |||||||||   :::   |||   ||||||||||||||||
Db        763 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 822

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
              |||||||||   |||   ||||||:::|||   |||:::|||      ::::::
Db        823 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 882

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
              ||||||||||||:::::::::||||||||||||||||   :::::::::||||||||||||
Db        883 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 942

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
                          :::::::::   ||||||:::   :::|||          |||:::
Db        943 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
                :::      :::         |||:::||||||:::|||   |||:::   |||:::
Db       1003 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1059

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
              |||   |||   ||||||   |||||||||   ||||||   ||||||:::|||||||||
Db       1060 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1119

Qy        324 Thr 324
              |||
Db       1120 ACC 1122

RESULT 8
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 38:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1263 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

Alignment Scores:
Pred. No.:                7.07e-72        Length:          1263
Score:                    637.50          Matches:         130
Percent Similarity:       54.85%          Conservative:    68
Best Local Similarity:    36.01%          Mismatches:      120
Query Match:              35.46%          Indels:          43
DB:                       4               Gaps:            6

US-09-980-881A-3 (1-338) x US-09-011-769A-38 (1-1263)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||:::      :::|||                              :::   ::::::
Db         58 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 117

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              :::   |||   :::|||   :::|||       |||:::|||   :::          |||
Db        118 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 177

Qy         41 ValLysLysLysGlnValHisPheProValAsnAlaSerAspValAspAsnValLysAla 60
                        |||   |||   |||   |||   |||          |||:::
Db        178 AAACCTCACAGTACAGTTGACTTCCGTGCTAAAGCAGAAGATACTGTCACTGTGGAGAAT 237

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
                 |||      :::   :::         ||||||:::::::::::::   :::::::::
Db        238 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 297

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              :::   |||      :::                ||||||:::          ||||||:::
Db        298 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 348

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              |||:::          |||   :::|||   :::   :::          :::|||
Db        349 TACAACAAGTGGGAAACGATAGAGGCTTCGACTCAACAAGTCGCCACTGAGAATCCAGCC 408

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ::::::::::::      ||||||:::::||||||         :::|||:::||||||
Db        409 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 468

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              |||   ||||||          |||   ||||||::::::|||||||||   ||||||
Db        469 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 525

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------------------- 173
              ||||||||||||||||||||||||||   ||||||:::
Db        526 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 585

Qy        173 ------------------------------------------------------------ 173

Db        586 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 645

Qy        174 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 183
                          |||:::                  :::|||   |||||||||   |||
Db        646 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 705

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
              |||   :::      :::   ||||||||||||||||   ||||||||||||
Db        706 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 762

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
              |||||||||   |||||||||   :::   |||   ||||||||||||||||
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```
Db        763 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 822

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243

Db        823 GCAGAGTCTGAAAAGGAAACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 882

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263

Db        883 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 942

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283

Db        943 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303

Db       1003 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1059

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323

Db       1060 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1119

Qy        324 Thr 324

Db       1120 ACC 1122

RESULT 9
US-08-860-882A-71
; Sequence 71, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear

US-08-860-882A-71

Alignment Scores:
Pred. No.:                7.27e-72      Length:          1284
Score:                    637.50        Matches:         130
Percent Similarity:       54.85%        Conservative:    68
Best Local Similarity:    36.01%        Mismatches:      120
Query Match:              35.46%        Indels:          43
DB:                       2             Gaps:            6

US-09-980-881A-3 (1-338) x US-08-860-882A-71 (1-1284)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

Db         85 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 144

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

Db        145 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 204

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60

Db        205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 264

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80

Db        265 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100

Db        325 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 375

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120

Db        376 TACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCC 435

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140

Db        436 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 495

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160

Db        496 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 552

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 173

Db        553 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 612

Qy        173 ---------- 173

Db        613 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 672

Qy        174 ------------GlyHis-----------------AsnArgMetTrpArgLysAsnArg 183

Db        673 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 732

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203

Db        733 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 789

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223

Db        790 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 849

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243

Db        850 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 909

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263

Db        910 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 969

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
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                          :::::::::   ||||||:::   :::|||          |||:::
Db        970 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
                 :::     :::      |||:::||||||:::|||   |||:::   |||:::
Db       1030 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1086

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
               |||   |||   ||||||   |||||||||   ||||||   ||||||:::|||||||||
Db       1087 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146

Qy        324 Thr 324
               |||
Db       1147 ACC 1149

RESULT 10
US-09-011-769A-55
; Sequence 55, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 55:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1284 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION: 1..1272
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION: 352..1272
;        SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-55

Alignment Scores:
Pred. No.:              7.27e-72        Length:         1284
Score:                  637.50          Matches:        130
Percent Similarity:     54.85%          Conservative:   68
Best Local Similarity:  36.01%          Mismatches:     120
Query Match:            35.46%          Indels:         43
DB:                     4               Gaps:           6

US-09-980-881A-3 (1-338) x US-09-011-769A-55 (1-1284)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||:::      :::|||                          :::   ::::::
Db         85 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 144

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              :::   |||   :::|||   :::|||      |||:::|||   :::         |||
Db        145 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 204

Qy         41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
                        |||  |||  |||  |||  |||         |||:::
Db        205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 264

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
                 |||      :::  :::         ||||||:::::::::::   :::::::::
Db        265 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              :::   |||      :::                |||||||::        |||||||:::
Db        325 GAGGCTCAGTTTGATAGCCGGGTT----------CGTGCAACAGGACACAGTTATGAGAAG 375

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              |||:::           |||  :::|||  :::  :::        :::|||
Db        376 TACAACAAGTGGGAAACGATAGAGGCTTCGACTCAACAAGTCGCCACTGAGAATCCAGCC 435

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              :::::::::::      ||||||:::::||||||        :::|||:::||||||
Db        436 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 495

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              |||   ||||||          |||   ||||||::::::|||||||||   ||||||
Db        496 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 552

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 173
              ||||||||||||||||||||||||||||||||||||||:::
Db        553 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 612

Qy        173 ---------- 173

Db        613 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 672

Qy        174 ----------GlyHis----------AsnArgMetTrpArgLysAsnArg 183
                        |||:::          :::|||   |||||||||   |||
Db        673 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 732

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
              |||   :::      :::   ||||||||||||||   ||||||||||||
Db        733 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 789

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
               |||||||||   |||||||||   :::   |||   ||||||||||||||
Db        790 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 849

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
              |||||||||   |||   ||||||:::|||   |||:::|||       ::::::
Db        850 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 909

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
              ||||||||||||:::::::::||||||||||||||   :::::::::||||||||||||
Db        910 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 969

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
                       :::::::::   ||||||:::   :::|||          |||:::
Db        970 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
                 :::      :::         |||:::||||||:::|||   |||:::   |||:::
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```
Db       1030 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1086

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323

Db       1087 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146

Qy        324 Thr 324

Db       1147 ACC 1149
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RESULT 11
US-09-023-655-1020
; Sequence 1020, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1020:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179933
US-09-023-655-1020

Alignment Scores:

Pred. No.:	1.09e-69	Length:	1622
Score:	622.00	Matches:	128
Percent Similarity:	55.12%	Conservative:	71
Best Local Similarity:	35.46%	Mismatches:	118
Query Match:	34.59%	Indels:	44
DB:	4	Gaps:	7

US-09-980-881A-3 (1-338) x US-09-023-655-1020 (1-1622)

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Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60

Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80

Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99

Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119

Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139

Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159

Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 173

Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        173 ---------- 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 ----------GlyHis----------AsnArgMetTrpArgLysAsn 182

Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202

Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222

Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242

Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerSer 262

Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282

Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302

Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322

Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323

Db       1123 TTT 1125
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RESULT 12

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US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
;  APPLICANT: Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0047-USA
;  CURRENT APPLICATION NUMBER: US/09/675,305
;  CURRENT FILING DATE:  2000-09-29
;  PRIOR APPLICATION NUMBER: US 60/156,685
;  PRIOR FILING DATE: 1999-09-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1311
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.:              1.59e-69        Length:         1311
Score:                  619.50          Matches:        136
Percent Similarity:     51.15%          Conservative:   64
Best Local Similarity:  34.78%          Mismatches:     127
Query Match:            34.45%          Indels:         64
DB:                     4               Gaps:           8

US-09-980-881A-3 (1-338) x US-09-675-305-9 (1-1311)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              :::         :::|||:::     :::|||:::|||      :::         |||
Db        109 TATGCTGGTGATAAAGTGATAAGATTTATTCCCAAAACAGAAGAGGAAGCATATGCACTG 168

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              :::   ::::::       ::::::   ||||||||||||   :::          :::
Db        169 AAGAAAATATCCTATCAACTTAAGGTGGACCTGTGGCAGCCCAGCAGTATCTCCTATGTA 228

Qy         41 ValLys------LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 58
                 :::              ||||||          |||   |||              :::
Db        229 TCAGAGGGAACAGTTACTGATGTCCATATCCCCCAAAATGGTTCCCGAGCC------CTG 282

Qy         59 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 78
              |||   |||      :::   |||         ||||||:::   |||::::::
Db        283 TTAGCCTTCTTACAGGAAGCCAACATCCAGTACAAGGTCCTCATAGAAGATCTTCAGAAA 342

Qy         79 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSer------ 96
              :::::::::      |||     |||          |||   |||   |||
Db        343 ACACTGGAGAAGGGAAGCAGCTTGCACACCCAGAGAAACCGAAGATCCCTCTCTGGATAT 402

Qy         97 TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGlu 116
              ||||||   ||||||||||||   ||||||   :::|||:::      :::   :::
Db        403 AATTATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAA 462

Qy        117 ArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeu 136
              |||      ::::::              ||||||   |||:::|||         |||
Db        463 ACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTT 522

Qy        137 TyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCys 156
              ::::::||||||:::   |||:::          |||   |||:::||||||||||||
Db        523 TTTATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGT 579

Qy        157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle--------- 173
              ||||||||||||||||||||||   ||||||||||   ||||||:::
Db        580 GGTATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCT 639

Qy        173 ------------------------------------------------------------ 173
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```
Db        640 CTTCTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTAT 699

Qy        174 ----------------------------------------GlyHisAsnArgMetTrp 179
                                                     ::::::|||   |||
Db        700 ATCATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGG 759

Qy        180 ArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsn 199
              ||||||   ||||||      :::          |||   |||   |||   |||||||||
Db        760 AGAAAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAAC 819

Qy        200 PheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyr 219
              :::      |||   ||||||:::|||||||||||          |||   :::||||||
Db        820 TGGAAAGTGAAG---TGGTGTGATGAAGCAGCTTCTATGCACCCTTGTGATGACACATAC 876

Qy        220 CysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArg 239
              ||||||   :::||||||||||||||||||||||||||||||||:::|||||||||:::
Db        877 TGTGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAA 936

Qy        240 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 259
              :::         |||:::||||||:::|||   |||:::|||:::|||   :::::::::
Db        937 CACAGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTAT 996

Qy        260 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSer 279
              ||||||||||||    :::          :::          :::          |||
Db        997 CCCTATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTAT 1056

Qy        280 GluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGly 299
              :::||||||   |||::::::                  ||||||   :::|||
Db       1057 AAAGCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCC 1113

Qy        300 SerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIle 319
              |||   |||||||||::::::   |||          ||||||   |||      |||||||
Db       1114 TCCACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATA 1173

Qy        320 LysTyrSerPhe----------------------------------------------- 323
                 |||:::|||
Db       1174 CCTTATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAG 1233

Qy        324 ----ThrSerAsnProProValGluLysLeu 332
                  :::|||||||||||||||:::||||||
Db       1234 ATGCTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 13
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
;  APPLICANT: Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0047-USA
;  CURRENT APPLICATION NUMBER: US/10/200,344
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: US/09/675,305
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1311
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.:              1.59e-69        Length:         1311
Score:                  619.50          Matches:        136
Percent Similarity:     51.15%          Conservative:   64
Best Local Similarity:  34.78%          Mismatches:     127
```

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Query Match:          34.45%      Indels:        64
DB:                   4           Gaps:          8

US-09-980-881A-3 (1-338) x US-10-200-344-9 (1-1311)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              :::     :::|||:::     :::|||:::|||      :::          |||
Db        109 TATGCTGGTGATAAAGTGATAAGATTTATTCCCAAAACAGAAGAGGAAGCATATGCACTG 168

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              :::   ::::::        ::::::   ||||||||||||   :::          :::
Db        169 AAGAAAATATCCTATCAACTTAAGGTGGACCTGTGGCAGCCCAGCAGTATCTCCTATGTA 228

Qy         41 ValLys------LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 58
                 :::                |||||          |||   |||            :::
Db        229 TCAGAGGGAACAGTTACTGATGTCCATATCCCCCAAAATGGTTCCCGAGCC------CTG 282

Qy         59 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 78
              |||   |||       :::   |||         ||||||:::   |||::::::
Db        283 TTAGCCTTCTTACAGGAAGCCAACATCCAGTACAAGGTCCTCATAGAAGATCTTCAGAAA 342

Qy         79 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSer------ 96
                 :::::::::      |||       |||         |||   |||   |||
Db        343 ACACTGGAGAAGGGAAGCAGCTTGCACACCCAGAGAAACCGAAGATCCCTCTCTGGATAT 402

Qy         97 TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGlu 116
              ||||||   ||||||||||||   ||||||   :::|||:::      :::   :::
Db        403 AATTATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAA 462

Qy        117 ArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeu 136
              |||     ::::::          ||||||   |||:::|||      |||
Db        463 ACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTT 522

Qy        137 TyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCys 156
              ::::::||||||:::   |||:::          |||   |||:::|||||||||||
Db        523 TTTATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGT 579

Qy        157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle--------- 173
              |||||||||||||||||||||||   ||||||||||   ||||||:::
Db        580 GGTATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCT 639

Qy        173 ------------------------------------------------------------ 173

Db        640 CTTCTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTAT 699

Qy        174 -----------------------------------------GlyHisAsnArgMetTrp 179
                                                        ::::::|||   |||
Db        700 ATCATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGG 759

Qy        180 ArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsn 199
              ||||||   ||||||      :::          |||   |||   |||   |||||||||
Db        760 AGAAAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAAC 819

Qy        200 PheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyr 219
              :::      |||   ||||||:::||||||||||||         |||   :::||||||
Db        820 TGGAAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATAC 876

Qy        220 CysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArg 239
              ||||||   :::||||||||||||||||||||||||||||||||:::||||||||||:::
Db        877 TGTGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAA 936

Qy        240 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 259
              :::         |||:::||||||:::|||   |||:::|||:::|||   :::::::::
Db        937 CACAGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTAT 996

Qy        260 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSer 279
              ||||||||||||      :::         :::         :::         |||
Db        997 CCCTATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTAT 1056

Qy        280 GluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGly 299
              :::||||||   |||::::::                ||||||   :::|||
Db       1057 AAAGCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCC 1113

Qy        300 SerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIle 319
              |||   |||||||||:::::::   |||          ||||||   |||      ||||||
Db       1114 TCCACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATA 1173

Qy        320 LysTyrSerPhe----------------------------------------------- 323
                 |||:::|||
Db       1174 CCTTATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAG 1233

Qy        324 ----ThrSerAsnProProValGluLysLeu 332
                  :::|||||||||||||||:::||||||
Db       1234 ATGCTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 14
US-09-171-945-124
; Sequence 124, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;  APPLICANT:  Emery, Stephen
;  APPLICANT:  Copley, Clive Graham
;  APPLICANT:  Edge, Michael Derek
;  TITLE OF INVENTION:  Monoclonal Antibody to CEA, Conjugates Comprising Said
;  TITLE OF INVENTION:  Antibody, and Their Therapeutic Use in an Adept System
;  FILE REFERENCE:  Monoclonal Antibody to CEA
;  CURRENT APPLICATION NUMBER: US/09/171,945
;  CURRENT FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  GB9703103.3
;  PRIOR FILING DATE:  1997-02-14
;  PRIOR APPLICATION NUMBER:  GB9609405.7
;  PRIOR FILING DATE:  1996-05-04
;  PRIOR APPLICATION NUMBER:  PCT/GB97/01165;
;  PRIOR FILING DATE:  1997-04-29
;  NUMBER OF SEQ ID NOS:  131
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 2154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-124

Alignment Scores:
Pred. No.:              3.74e-69      Length:          2154
Score:                  619.50        Matches:         127
Percent Similarity:     54.29%        Conservative:    69
Best Local Similarity:  35.18%        Mismatches:      122
Query Match:            34.45%        Indels:          43
DB:                     3             Gaps:            6

US-09-980-881A-3 (1-338) x US-09-171-945-124 (1-2154)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||:::     :::|||                                  :::   ::::::
Db         64 TTTGAAGGCGAGAAGGTGTTCCGTGTTAACGTTGAAGATGAAAATCACATTAACATAATC 123

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              :::   |||   :::|||   :::|||      |||:::|||   :::          |||
Db        124 CGCGAGTTGGCCAGCACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 183

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                        |||   |||   |||   |||   |||          |||:::
Db        184 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAAT 243

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              |||       :::   :::          ||||||:::::::::::   :::::::::
Db        244 GTTCTAAAGCAGAATGAACTACAATACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 303

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              :::   |||       :::                ||||||:::          ||||||:::
Db        304 GAGGCTCAGTTTGATAGCCGGGTT---------CGTGCAACAGGACACAGTTATGAGAAG 354

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              |||:::            |||   :::|||   :::   :::         :::|||
```

```
Db        355 TACAACAAGTGGGAAACGATAGAGGCTTGGACTCAACAAGTCGCCACTGAGAATCCAGCC 414

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              :::::::::::      ||||||:::::||||||         :::|||:::||||||
Db        415 CTCATCTCTCGCAGTGTTATCGGAACCACATTTGAGGGACGCGCTATTTACCTCCTGAAG 474

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              |||   ||||||           |||   ||||||::::::|||||||   ||||||
Db        475 GTT---GGCAAAGCTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 531

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------------------- 173
              ||||||||||||||||||||||||||||   ||||||:::
Db        532 AGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTTGTAAGAGAGGCTGTTCGTACCTAT 591

Qy        173 ------------------------------------------------------------ 173

Db        592 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCTGTG 651

Qy        174 ------------GlyHis------------------AsnArgMetTrpArgLysAsnArg 183
                          |||:::                  :::|||   |||||||||   |||
Db        652 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 711

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
              |||  :::      :::   ||||||||||||||   ||||||||||||
Db        712 TCCACCCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT 768

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
              |||||||||   |||||||||   :::   |||   ||||||||||||||||
Db        769 GGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 828

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
              |||||||||   |||   ||||||:::|||   |||:::|||      ::::::
Db        829 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCCGCAACAAACTCTCTTCC 888

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
              ||||||||||||:::::::::||||||||||||||   :::::::::||||||||||||
Db        889 ATCAAGGCATATCTGACAATCCACTCGTACTCCCAAATGATGATCTACCCTTACTCATAT 948

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
                          :::::::::   ||||||:::   :::|||          |||:::
Db        949 GCTTACAAACTCGGTGAGAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1008

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
              :::   :::   |||:::||||||:::|||   |||:::   |||:::
Db       1009 GAACTT---GCCTCACTGCACGGCACCAAGTACACATATGGCCCGGGAGCTACAACAATC 1065

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
              |||   :::   |||          ||||||   ||||||   |||||:::|||||||||
Db       1066 TATCCTTCTGCTGGGACTTCTAAAGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1125

Qy        324 Thr 324
              |||
Db       1126 ACC 1128

RESULT 15
US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
;  GENERAL INFORMATION:
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Fulga, Netta
;    APPLICANT:  Mendelovitch, Simona
;    APPLICANT:  Gorecki, Marian
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/782,760
;      FILING DATE:  13-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/378,233
;      FILING DATE:  25-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  927 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..927
US-08-782-760-5

Alignment Scores:
Pred. No.:                1.47e-68        Length:          927
Score:                    610.00          Matches:         126
Percent Similarity:       60.50%          Conservative:    44
Best Local Similarity:    44.84%          Mismatches:      71
Query Match:              33.93%          Indels:          41
DB:                       2               Gaps:            5

US-09-980-881A-3 (1-338) x US-08-782-760-5 (1-927)

Qy         93 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 112
              ||||||          |||   :::|||::::::          |||   :::||||||:::
Db          1 GCAAGTGGACACAGCTACACCAAGTACACACAACTGGGAAACGATTGAGGCGTGGATTCAA 60

Qy        113 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 132
                 :::         :::||||||::::::|||:::      ||||||::::::||||||
Db         61 CAAGTTGCCACTGATAATCCAGACCTTGTCACTCAGAGCGTCATTGGAACCACATTTGAA 120

Qy        133 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 152
                    :::||||||||||||:::   ||||||   :::       |||   ||||||
Db        121 GGACGTAACATGTATGTCCTCAAGATT---GGTAAAACTAGACCGAATAAGCCTGCCATC 177

Qy        153 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 172
              :::||||||||||||   ||||||||||||||||||||||||||||||   ||||||
Db        178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTTCTCCTGCATTCTGTCAGTGGTTT 237

Qy        173 Ile---------------------------------------------------------- 173
              :::
Db        238 GTGAGAGAGGCTGTCCGTACCTATAATCAAGAGATCCACATGAAACAGCTTCTAGATGAA 297

Qy        174 ----------------------------------GlyHis------------------- 175
                                                 |||:::
Db        298 CTGGATTTCTATGTTCTGCCTGTGGTCAACATTGATGGCTATGTCTACACCTGGACTAAG 357

Qy        176 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 195
              :::||||||||||||||   ||||||      |||   :::   |||:::|||   |||
Db        358 GACAGAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGAC 417

Qy        196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 215
                 ||||||||||||   :::      | |||||||   |||||||||   |||   |||
```

```
Db        418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy        216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235
              ||||||||||||||||||      ||||||||||||    |||   ||||||:::|||
Db        475 TCTGAAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534

Qy        236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255
              |||:::|||   |||::::::   ||||||||||||:::::::::|||||||||||||||
Db        535 TTCATCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAG 594

Qy        256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275
                 :::::::::|||||||||||               :::::::::||||||||:::
Db        595 ATGATGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

Qy        276 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295
                 :::         |||   :::   :::      |||         |||:::||||||
Db        655 GCCCTGGTGAAAGGTGCGGCAAAGGAGCTT---GCCACTCTGCATGGCACCAAGTACACA 711

Qy        296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 315
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db        712 TATGGCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTAT 771

Qy        316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 335
              |||   ||||||||||||||||||||          |||      :::||||||   |||
Db        772 GATCAGGGAATCAAATATTCCTTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830

Qy        336 Ser 336
              |||
Db        831 TCT 833
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Job time : 110.464 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 588.636 Seconds
(without alignments)
2944.316 Million cell updates/sec

Title: US-09-980-881A-3
Perfect score: 1798
Sequence: 1 FQSGQVLAALPRTSRQVQVL.....IKYSFTSNPPVEKLLPLSLK 338

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09980881_@CGN_1_1_811_@runat_28102004_131644_12110
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1749.5	97.3	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1749.5	97.3	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1732	96.3	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1708.5	95.0	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1708.5	95.0	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1628	90.5	1272	15	US-10-379-836-1	Sequence 1, Appli
7	1329.5	73.9	1037	16	US-10-115-479-63	Sequence 63, Appl
8	1290.5	71.8	1132	16	US-10-115-479-65	Sequence 65, Appl
9	902	50.2	1400	9	US-09-925-302-24	Sequence 24, Appl
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11	622	34.6	1254	14	US-10-229-546-3	Sequence 3, Appli
12	622	34.6	1622	14	US-10-229-546-1	Sequence 1, Appli
13	622	34.6	1622	15	US-10-429-802-21	Sequence 21, Appl
14	622	34.6	1622	16	US-10-430-503-12	Sequence 12, Appl
15	622	34.6	1622	16	US-10-262-511-71	Sequence 71, Appl
16	622	34.6	1622	16	US-10-641-643-1020	Sequence 1020, Ap
17	622	34.6	1633	15	US-10-341-434-187	Sequence 187, App
18	622	34.6	1740	14	US-10-116-802-95	Sequence 95, Appl
19	619.5	34.5	1302	17	US-10-477-515-1	Sequence 1, Appli
20	619.5	34.5	1311	13	US-10-200-344-9	Sequence 9, Appli
21	619.5	34.5	1993	15	US-10-274-639-33	Sequence 33, Appl
22	619.5	34.5	1993	16	US-10-333-574-33	Sequence 33, Appl
23	619.5	34.5	2154	9	US-09-910-059-124	Sequence 124, App
24	618	34.4	1332	9	US-09-954-456-1141	Sequence 1141, Ap
25	617.5	34.3	1907	18	US-10-757-262-127	Sequence 127, App
26	591	32.9	416	9	US-09-960-352-14595	Sequence 14595, A
27	571.5	31.8	2128	13	US-10-200-344-13	Sequence 13, Appl
28	569	31.6	1125	9	US-09-888-615-2	Sequence 2, Appli
29	569	31.6	1332	15	US-10-176-306-75	Sequence 75, Appl
30	569	31.6	1603	15	US-10-176-306-73	Sequence 73, Appl
31	562	31.3	1826	15	US-10-252-157-453	Sequence 453, App
32	554	30.8	1200	14	US-10-200-910-7	Sequence 7, Appli
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34	549	30.5	1870	9	US-09-910-059-112	Sequence 112, App
35	549	30.5	1870	17	US-10-608-710-3	Sequence 3, Appli
36	534.5	29.7	1050	13	US-10-200-344-11	Sequence 11, Appl
37	533.5	29.7	991	16	US-10-383-201-93	Sequence 93, Appl
38	527.5	29.3	1260	16	US-10-257-174-16	Sequence 16, Appl
39	527.5	29.3	1311	14	US-10-200-910-5	Sequence 5, Appli
40	527.5	29.3	1311	16	US-10-257-174-15	Sequence 15, Appl
41	527.5	29.3	1311	17	US-10-451-821-1	Sequence 1, Appli
42	527.5	29.3	1311	18	US-10-843-130-5	Sequence 5, Appli
43	527.5	29.3	1348	16	US-10-072-012-315	Sequence 315, App
44	527.5	29.3	1641	17	US-10-381-820A-5	Sequence 5, Appli
45	523.5	29.1	1295	17	US-10-363-829-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

Pred. No.:	6.31e-206	Length:	1625
Score:	1749.50	Matches:	336
Percent Similarity:	94.38%	Conservative:	0
Best Local Similarity:	94.38%	Mismatches:	2
Query Match:	97.30%	Indels:	18
DB:	9	Gaps:	1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

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Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
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Db        563 AGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATAATCGAATGTGGAGA 622

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RESULT 2
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; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores:

Pred. No.:	6.31e-206	Length:	1625
Score:	1749.50	Matches:	336
Percent Similarity:	94.38%	Conservative:	0
Best Local Similarity:	94.38%	Mismatches:	2
Query Match:	97.30%	Indels:	18
DB:	14	Gaps:	1

US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

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Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
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Qy        181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200
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Db        623 AAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTT 682

Qy        201 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220
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Db        683 GCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGT 742

Qy        221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 240
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Db        743 GGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAAT 802

Qy        241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260
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Qy        321 TyrSerPhe---------------------------------------------------- 323
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Db       1043 TATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGT 1102

Qy        324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
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RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
;   LENGTH: 1728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

Alignment Scores:
Pred. No.:              1.03e-203       Length:         1728
Score:                  1732.00         Matches:        338
Percent Similarity:     86.01%          Conservative:   0
Best Local Similarity:  86.01%          Mismatches:     0
Query Match:            96.33%          Indels:         55
DB:                     9               Gaps:           2
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US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)

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Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
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Db        146 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 205

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
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Db        206 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 265

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
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Db        266 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 325

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
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Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
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Db        386 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 445

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
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Db        446 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 505

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
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Qy        175 ------------------------------------------------------------ 175

Db        626 GGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 685

Qy        176 ----------------------------------AsnArgMetTrpArgLysAsnArg 183
                                                 ||||||||||||||||||||||
Db        686 GTTAATGTGGACGGTTATGACTACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGT 745

Qy        184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAA 805

Qy        204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT 865

Qy        224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 CCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAG 925

Qy        244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCATATTCCTAT 985

Qy        264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        986 ACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1045

Qy        284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 GCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1105

Qy        304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1106 TACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1165

Qy        324 ----------------------------------------------------ThrSerAs 326
                                                                   ||||||||
Db       1166 ACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAA 1225

Qy        326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
               ||||||||||||||||||||||||||||||||||||
Db       1226 CCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1262

RESULT 4
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.:                5.59e-201       Length:          1344
Score:                    1708.50         Matches:         336
Percent Similarity:       84.42%          Conservative:    0
Best Local Similarity:    84.42%          Mismatches:      2
Query Match:              95.02%          Indels:          60
DB:                       16              Gaps:            3

US-09-980-881A-3 (1-338) x US-10-115-479-69 (1-1344)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 156

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 216

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 276

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 336

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 396

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 456

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        457 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 516

Qy        141 ----------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155
                      |||||||||||||| ||||  ||||||||||||||||||||||||
Db        517 GGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGAC 576

Qy        156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        577 TGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT 636

Qy        175 ------------------------------------------------------------ 175

Db        637 ATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTC 696

Qy        176 ----------------------------------------------------AsnArgMet 178
                                                                   ||||||||
Db        697 TATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAATCGAATG 756

Qy        179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        757 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 816

Qy        199 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 218
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        817 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 876

Qy        219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        877 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 936

Qy        239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 996
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Qy        259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 1056

Qy        279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db       1057 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 1116

Qy        299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1176

Qy        319 IleLysTyrSerPhe---------------------------------------------- 323
              ||||||||||||||
Db       1177 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1236

Qy        324 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
                    ||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:
Pred. No.:              8.55e-201       Length:         1743
Score:                  1708.50         Matches:        336
Percent Similarity:     84.42%          Conservative:   0
Best Local Similarity:  84.42%          Mismatches:     2
Query Match:            95.02%          Indels:         60
DB:                     16              Gaps:           3

US-09-980-881A-3 (1-338) x US-10-115-479-67 (1-1743)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 145

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 205

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 265

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 325

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 385

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 445

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 505

Qy        141 ---------------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155
                            ||||||||||||||||||  ||||||||||||||||||||||
Db        506 GGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGAC 565

Qy        156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT 625

Qy        175 ------------------------------------------------------------ 175

Db        626 ATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTC 685

Qy        176 ----------------------------------------------------AsnArgMet 178
                                                                   ||||||||
Db        686 TATGTTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAATCGAATG 745

Qy        179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 805
```

```
Qy       199 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 218
Db       806 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 865

Qy       219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238
Db       866 TACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGA 925

Qy       239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258
Db       926 AGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTG 985

Qy       259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278
Db       986 TTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCC 1045

Qy       279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298
Db      1046 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 1105

Qy       299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 318
Db      1106 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 1165

Qy       319 IleLysTyrSerPhe--------------------------------------------- 323
Db      1166 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1225

Qy       324 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db      1226 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1277
```

RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

Alignment Scores:

Pred. No.:	4.86e-191	Length:	1272
Score:	1628.00	Matches:	318
Percent Similarity:	83.21%	Conservative:	9
Best Local Similarity:	80.92%	Mismatches:	11
Query Match:	90.55%	Indels:	55
DB:	15	Gaps:	2

US-09-980-881A-3 (1-338) x US-10-379-836-1 (1-1272)

```
Qy         1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db        67 TTTCAGAGTGGCCAGGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTGCTA 126

Qy        21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db       127 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCGGACCTTATT 186

Qy        41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db       187 GAGAAGAAAAAACAAGTCCATTTTTTTGTAAATTCATCTGATGTCGACAATGTGAAAGCC 246

Qy        61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db       247 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCCTGCTGGCAGATGTGGAAGATCTTATT 306

Qy        81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db       307 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 366

Qy       101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db       367 TATCACTCACTAAATGAAATCTATTCTTGGATAGAACTTATAACTGAGAAGTATCCTGAT 426

Qy       121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db       427 ATGCTTACAAAAATCCACATTGGATCCTCCTATGAGAAGCACCCACTTTATGTTTTAAAG 486

Qy       141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db       487 GTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATGTGGATTGACTGTGGAATCCATGCC 546

Qy       161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis---------------- 175
Db       547 AGAGAATGGATCTCCCCTGCTTTCTGCTTGTGGTTCATAGGCCATATAACTGAATACTAC 606

Qy       175 ------------------------------------------------------------ 175
Db       607 GGGATAATAGGGGAATATACCAATCTTCCGAGGCATGTGGATTTCTATGTTATGCCAGTG 666

Qy       176 ----------------------------------AsnArgMetTrpArgLysAsnArg 183
Db       667 GTTAATGTGGATGGTTATGACTACTCATCGAAAAAGAATCGAATGTGGAGAAAGAACCGT 726

Qy       184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db       727 TCTTTCTATGCGAACAATCGTTGCATCGGAACAGACCTGAACAGGAACTTTGCGTCCAAA 786

Qy       204 HisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db       787 CACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGCTCGGAAACCTACTGTGGACTTTAT 846

Qy       224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db       847 CCTGAGTCAGAACCAGAAGCGAAGGCGGTGGCTAATTTCTTGAGAAGAAATATCAACCAC 906

Qy       244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSerTyr 263
Db       907 ATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATCGTGTTTCCATATTCCTAT 966

Qy       264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db       967 ACTCGAAGCAAAAGCAAAGACCACGAGGAATTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1026

Qy       284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db      1027 GCTATTCAGAAAACCAGTAAAAATATCACGTATACACATGGCCGTGGCTCAGAAACCTTA 1086

Qy       304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db      1087 TACCTAGCTCCTGGAGGTGCGGACGATTGGATCTATGATTTGGGCATCAAATATTCGTTT 1146

Qy       324 ------------------------------------------------------ThrSerAs 326
Db      1147 ACAATTGAACTTCGAGATACGGGCAAATACGGATTCTTGCTGCCTGAGCGTTACATCAAA 1206

Qy       326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
Db      1207 CCCACTTGTAAAGACGCTTTTGCCGCTGTCTCTAAAA 1243
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RESULT 7
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.:              3.48e-154      Length:          1037
Score:                  1329.50        Matches:         272
Percent Similarity:     76.40%         Conservative:    0
Best Local Similarity:  76.40%         Mismatches:      2
Query Match:            73.94%         Indels:          82

DB:                     16             Gaps:            2

US-09-980-881A-3 (1-338) x US-10-115-479-63 (1-1037)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTGAAAGCC 286

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 346

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 466

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 ATGCTTACAAAAATCCACATCGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 526

Qy        141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
              ||||||||||||||||||  ||||||||||||||||||||||
Db        527 GTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGAC---------------- 571

Qy        161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180

Db        571 ------------------------------------------------------------ 571

Qy        181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200

Db        571 ------------------------------------------------------------ 571

Qy        201 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220
                                                                      |||
Db        572 ------------------------------------------------------TGT 574

Qy        221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAGAAAT 634

Qy        241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTTTCCA 694

Qy        261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 TATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAA 754

Qy        281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        755 GCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCATGGCTCA 814

Qy        301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 GAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCATCAAA 874

Qy        321 TyrSerPhe---------------------------------------------------- 323
              |||||||||
Db        875 TATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGAGCGT 934

Qy        324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
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                 ||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 TACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 980

RESULT 8
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
;   LENGTH: 1132
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.:              2.74e-149      Length:        1132
Score:                  1290.50        Matches:       263
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Percent Similarity:     66.08%         Conservative:  0
Best Local Similarity:  66.08%         Mismatches:    1
Query Match:            71.77%         Indels:        134
DB:                     16             Gaps:          4

US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 TTTCAGAGTGGCCAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GTGAAGAAAAAACAAGTCCATTTTTTTGTCAAATGCATCTGATGTCGACAATGTGAAAGCC 286

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 CATTTAAATGTGAGCGGAATTCCATGCAGTGTCTTGCTGGCAGACGTGGAAGATCTTATT 346

Qy         81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 CAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406

Qy        101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGGCATCCTGAT 466

Qy        121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 ATGCTTACAAAAATCCACATTGGATCCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 526

Qy        141 ----------ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155
                       ||||||||||||||||||  ||||||||||||||||||||||
Db        527 GGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATATGGATTGAC 586

Qy        156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 TGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCAT 646

Qy        175 ------------------------------------------------------------ 175

Db        647 ATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTC 706

Qy        176 ----------------------------------------------------------AsnArgMet 178
                                                                         ||||||||
Db        707 TATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAATCGAATG 766

Qy        179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 TGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGG 826

Qy        199 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 886

Qy        219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238
              ||||||||||||||||||||
Db        887 TACTGTGGACTTTATCCTGAG---------------------------------------- 907

Qy        239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258

Db        907 ------------------------------------------------------------ 907

Qy        259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278

Db        907 ------------------------------------------------------------ 907

Qy        279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298
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Db        907 ------------------------------------------------------------ 907

Qy        299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 ---TCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGC 964

Qy        319 IleLysTyrSerPhe---------------------------------------------- 323
              ||||||||||||||
Db        965 ATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1024

Qy        324 -------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
                    ||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1076

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.:          5.54e-101      Length:          1400
Score:              902.00         Matches:         181
Percent Similarity: 76.05%         Conservative:    0
Best Local Similarity: 76.05%      Mismatches:      1
Query Match:        50.17%         Indels:          56
DB:                 9              Gaps:            2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy        157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy        175 ------------------------------------------------------------ 175

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy        176 ----------------------------------------------------AsnArgMetTr 179
                                                                   ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189

Qy        179 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        199 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        299 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        319 eLysTyrSerPhe---------------------------------------------- 323
              ||||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
                   ||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 719

RESULT 10
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.:          5.54e-101      Length:          1400
Score:              902.00         Matches:         181
Percent Similarity: 76.05%         Conservative:    0
Best Local Similarity: 76.05%      Mismatches:      1
Query Match:        50.17%         Indels:          56
DB:                 10             Gaps:            2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy        157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy        175 ------------------------------------------------------------ 175

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy        176 ----------------------------------------------------AsnArgMetTr 179
                                                                   ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189
```

```
Qy        179 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        199 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        299 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        319 eLysTyrSerPhe---------------------------------------------- 323
              |||||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
                   ||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 719

RESULT 11
US-10-229-546-3
; Sequence 3, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
;  APPLICANT: Weich, Nadine S.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREFOR
;  FILE REFERENCE: MPI01-156P1RNM
;  CURRENT APPLICATION NUMBER: US/10/229,546
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: 60/316,575
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1254
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1254)
US-10-229-546-3

Alignment Scores:
Pred. No.:              2.35e-66      Length:          1254
Score:                  622.00        Matches:         128
Percent Similarity:     55.12%        Conservative:    71
Best Local Similarity:  35.46%        Mismatches:      118
Query Match:            34.59%        Indels:          44
DB:                     14            Gaps:            7

US-09-980-881A-3 (1-338) x US-10-229-546-3 (1-1254)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60

Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80

Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99

Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119

Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139

Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159

Db        472 AAGATT---GGGGAAAAGAATGAAAGAACAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------------ 173

Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        173 ------------------------------------------------------------ 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 182

Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202

Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222

Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242

Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 262

Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282

Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302

Db       1006 GATGTTCTA---TCAACTCGATATGAAACCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322

Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323
              |||

Db       1123 TTT 1125
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Db       1123 TTT 1125

RESULT 12
US-10-229-546-1
; Sequence 1, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
;  APPLICANT: Weich, Nadine S.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREFOR
;  FILE REFERENCE: MPI01-156P1RNM
;  CURRENT APPLICATION NUMBER: US/10/229,546
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: 60/316,575
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1254)
US-10-229-546-1

Alignment Scores:
Pred. No.:              3.58e-66      Length:          1622
Score:                  622.00        Matches:         128
Percent Similarity:     55.12%        Conservative:    71
Best Local Similarity:  35.46%        Mismatches:      118
Query Match:            34.59%        Indels:          44
DB:                     14            Gaps:            7

US-09-980-881A-3 (1-338) x US-10-229-546-1 (1-1622)

Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||:     :::|||       |||:::     :::|||      ::::::
Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ::::::|||      |||   |||:::     |||   |||              :::
Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                          |||   |||   |||:::     :::         :::::::::
Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              |||:::   :::   :::       :::|||:::   |||:::::::::   |||
Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
              :::::|||           :::   :::       |||   |||          |||
Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119
              :::|||::::::      :::|||   :::|||   |||   :::   :::::::::|||
Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
              :::|||:::::::::|||   |||||||||:::   |||       ||||||||||||||
Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
              |||:::   |||::::::          :::   ||||||::::::|||||||||||||||
Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------------ 173
              ||||||||||||:::||||||||||||||||   ||||||:::
Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        173 ------------------------------------------------------------ 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 182
                           |||:::                 ||||||||||||||||||
Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
              ||||||          |||:::   ||||||||||||||||||||||||||||   :::
Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222
                 |||                 ::::::      |||::::::   |||   |||
Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
              ||||||||||||   |||   ||||||||   :::|||:::|||   ::::::|||
Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 262
              :::||||||   ||||||:::   ||||||||||||||   ::::::||||||||
Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
              ||||||                 :::||||||:::|||:::   ||||||
Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
                    :::   |||         |||||||||   :::|||                |||
Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
              :::|||          |||         ||||||   ||||||||||||||||||:::::
Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323
              |||
Db       1123 TTT 1125

RESULT 13
US-10-429-802-21
; Sequence 21, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: 60/377,672
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 1622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-802-21

Alignment Scores:
Pred. No.:              3.58e-66      Length:          1622
Score:                  622.00        Matches:         128
Percent Similarity:     55.12%        Conservative:    71
Best Local Similarity:  35.46%        Mismatches:      118
Query Match:            34.59%        Indels:          44
DB:                     15            Gaps:            7

US-09-980-881A-3 (1-338) x US-10-429-802-21 (1-1622)
```

```
Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||          :::|||          |||:::      :::|||      ::::::
Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ::::::|||      |||   |||:::      |||   |||             :::
Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                        |||   |||   |||:::      :::         :::::::::
Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              |||:::   :::   :::          :::|||:::   |||:::::::::   |||
Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
              :::::::|||          :::   :::      |||   |||         |||
Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119
              :::|||::::::      :::|||   :::|||   |||   :::   ::::::::|||
Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
              :::|||:::::::::|||   |||||||||:::   |||       |||||||||||||
Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
              |||:::   |||::::::          :::   ||||||::::::|||||||||||||||
Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----------------- 173
              ||||||||||||:::|||||||||||||||   ||||||:::
Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        173 ------------------------------------------------------------ 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 182
                           |||:::                 ||||||||||||||||||||
Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
              ||||||          |||:::   |||||||||||||||||||||||||||||   :::
Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222
                    |||          ::::::      |||::::::   |||   |||
Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
              ||||||||||||   |||   |||||||||   :::|||:::|||   :::::::|||
Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262
              :::|||||   ||||||:::   ||||||||||||||   ::::::|||||||||
Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
              ||||||          :::|||||:::|||:::   ||||||
Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
                  :::      |||          |||||||||   :::|||                |||
Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
              :::|||          |||          ||||||   ||||||||||||||||||::::::
Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323
```

```
                |||
Db       1123 TTT 1125

RESULT 14
US-10-430-503-12
; Sequence 12, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  LAN, KENG-LI
;  APPLICANT:  OU-YANG, FU
;  APPLICANT:  LIU, JAW-CHING
;  APPLICANT:  LAN, KENG-HSIN
;  TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
;  TITLE OF INVENTION:  REAGENTS
;  FILE REFERENCE: UTSC:797US
;  CURRENT APPLICATION NUMBER: US/10/430,503
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: 60/383,063
;  PRIOR FILING DATE: 2002-05-06
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 1622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-430-503-12

Alignment Scores:
Pred. No.:                3.58e-66      Length:          1622
Score:                    622.00        Matches:         128
Percent Similarity:       55.12%        Conservative:    71
Best Local Similarity:    35.46%        Mismatches:      118
Query Match:              34.59%        Indels:          44
DB:                       16            Gaps:            7

US-09-980-881A-3 (1-338) x US-10-430-503-12 (1-1622)
```

```
Qy          1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
              |||          :::|||          |||:::      :::|||      ::::::
Db         61 TTTGACAGGGAGAAGGTGTTCCGCGTGAAGCCCCAGGATGAAAAACAAGCAGACATCATA 120

Qy         21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
              ::::::|||      |||   |||:::      |||   |||             :::
Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                        |||   |||   |||:::      :::         :::::::::
Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
              |||:::   :::   :::          :::|||:::   |||:::::::::   |||
Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
              :::::::|||          :::   :::      |||   |||         |||
Db        301 GAGAAACAGTTTGATGTTAAAGAAGATATCCCAGGCAGGCACAGC---------TACGCA 351

Qy        100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119
              :::|||::::::      :::|||   :::|||   |||   :::   ::::::::|||
Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
              :::|||:::::::::|||   |||||||||:::   |||       |||||||||||||
Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
              |||:::   |||::::::          :::   ||||||::::::|||||||||||||||
Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----------------- 173
              ||||||||||||:::|||||||||||||||   ||||||:::
Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588
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Qy        173 ------------------------------------------------------------ 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 182
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Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
              ||||||         |||:::  ||||||||||||||||||||||||||||   :::
Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222
                    |||                 ::::::      |||::::::   |||   |||
Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
                |||||||||||   |||   |||||||||   :::|||:::|||   ::::::|||
Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 262
              :::||||||   ||||||:::   ||||||||||||||   ::::::||||||||||
Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
              ||||||                  :::||||||:::|||:::   ||||||
Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
                  :::      |||         |||||||||   :::|||                |||
Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
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Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323
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Db       1123 TTT 1125
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RESULT 15
US-10-262-511-71
; Sequence 71, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 71
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1251)
US-10-262-511-71

Alignment Scores:

Pred. No.:	3.58e-66	Length:	1622
Score:	622.00	Matches:	128
Percent Similarity:	55.12%	Conservative:	71
Best Local Similarity:	35.46%	Mismatches:	118
Query Match:	34.59%	Indels:	44
DB:	16	Gaps:	7

US-09-980-881A-3 (1-338) x US-10-262-511-71 (1-1622)

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              ::::::|||      |||  |||:::     |||  |||                :::
Db        121 AAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCACGTA 180

Qy         41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
                         |||   |||   |||:::     :::      :::::::::
Db        181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240

Qy         61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
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Db        241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300

Qy         81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
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Db        352 AAATACAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411

Qy        120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
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Db        412 GAAATGGTCTCTCGTATTAAAATTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471

Qy        140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159

Db        472 AAGATT---GGGGAAAAGAATGAAAGAAGAAAGGCTATTTTTATGGATTGTGGCATTCAC 528

Qy        160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------------ 173

Db        529 GCACGAGAATGGGTCTCCCCAGCATTCTGCCAGTGGTTTGTCTATCAGGCAACCAAAACT 588

Qy        173 ------------------------------------------------------------ 173

Db        589 TATGGGAGAAACAAAATTATGACCAAACTCTTGGACCGAATGAATTTTTACATTCTTCCT 648

Qy        174 --------------GlyHis-----------------AsnArgMetTrpArgLysAsn 182

Db        649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAAT 708

Qy        183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202

Db        709 CGTTCCAAGAACCAAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765

Qy        203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222

Db        766 GCTTCATGGAACTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825

Qy        223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242

Db        826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTCATTAGAAGCCACCTGAAT 885

Qy        243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValProTyrSer 262

Db        886 GAAATCAAGGTTTACATCACCTTCCATTCCTACTCCCAGATGCTATTGTTTCCCTATGGA 945

Qy        263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282

Db        946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAAGATTGGCACT 1005

Qy        283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302

Db       1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGGCCCAATAGAATCAACA 1062

Qy        303 LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322

Db       1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAAACACACA 1122

Qy        323 Phe 323

Db       1123 TTT 1125


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Job time : 599.636 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:34:50 ; Search time 18.7627 Seconds
(without alignments)
869.503 Million cell updates/sec

Title: US-09-980-881A-4
Perfect score: 1338
Sequence: 1 ASASYYEQYHSLNEIYSWIE.....IKYSFTSNPPVEKLLPLSLK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1257	93.9	386	4	US-09-813-133A-2	Sequence 2, Appli
2	1239.5	92.6	423	1	US-07-649-591B-3	Sequence 3, Appli
3	1239.5	92.6	423	1	US-08-277-540-3	Sequence 3, Appli
4	1239.5	92.6	423	1	US-08-430-787A-3	Sequence 3, Appli
5	1239.5	92.6	423	2	US-08-869-057-2	Sequence 2, Appli
6	1228.5	91.8	423	4	US-09-813-133A-4	Sequence 4, Appli
7	610	45.6	307	2	US-08-782-760-6	Sequence 6, Appli
8	610	45.6	307	5	PCT-US96-00995-6	Sequence 6, Appli
9	582	43.5	306	1	US-08-696-139-4	Sequence 4, Appli
10	582	43.5	404	1	US-08-696-139-2	Sequence 2, Appli
11	567	42.4	329	4	US-09-011-769A-51	Sequence 51, Appl
12	567	42.4	349	4	US-09-011-769A-47	Sequence 47, Appl
13	567	42.4	415	2	US-08-860-882A-57	Sequence 57, Appl
14	567	42.4	415	4	US-09-011-769A-39	Sequence 39, Appl
15	567	42.4	424	4	US-09-011-769A-56	Sequence 56, Appl
16	561	41.9	417	1	US-07-649-591B-7	Sequence 7, Appli
17	561	41.9	417	1	US-08-277-540-7	Sequence 7, Appli
18	561	41.9	417	1	US-08-430-787A-7	Sequence 7, Appli
19	560	41.9	349	4	US-09-011-769A-60	Sequence 60, Appl
20	559	41.8	349	4	US-09-011-769A-64	Sequence 64, Appl
21	554	41.4	396	1	US-07-649-591B-4	Sequence 4, Appli
22	554	41.4	396	1	US-08-277-540-4	Sequence 4, Appli
23	554	41.4	396	1	US-08-430-787A-4	Sequence 4, Appli
24	552	41.3	417	1	US-07-649-591B-6	Sequence 6, Appli
25	552	41.3	417	1	US-08-277-540-6	Sequence 6, Appli
26	552	41.3	417	1	US-08-430-787A-6	Sequence 6, Appli
27	552	41.3	417	4	US-09-917-254-66	Sequence 66, Appl
28	549	41.0	437	4	US-09-675-305-10	Sequence 10, Appl
29	549	41.0	437	4	US-10-200-344-10	Sequence 10, Appl
30	549	41.0	613	3	US-09-171-945-113	Sequence 113, App
31	549	41.0	716	3	US-09-171-945-125	Sequence 125, App
32	492	36.8	399	4	US-09-710-099-8	Sequence 8, Appli
33	492	36.8	399	4	US-10-200-910-8	Sequence 8, Appli
34	487.5	36.4	419	1	US-07-649-591B-5	Sequence 5, Appli
35	487.5	36.4	419	1	US-08-277-540-5	Sequence 5, Appli
36	487.5	36.4	419	1	US-08-430-787A-5	Sequence 5, Appli
37	483	36.1	417	1	US-07-649-591B-8	Sequence 8, Appli
38	483	36.1	417	1	US-08-277-540-8	Sequence 8, Appli
39	483	36.1	417	1	US-08-430-787A-8	Sequence 8, Appli
40	471.5	35.2	350	4	US-09-675-305-12	Sequence 12, Appl
41	471.5	35.2	350	4	US-10-200-344-12	Sequence 12, Appl
42	465.5	34.8	419	3	US-08-640-906-2	Sequence 2, Appli
43	465.5	34.8	419	3	US-09-395-936-2	Sequence 2, Appli
44	465.5	34.8	436	4	US-09-710-099-6	Sequence 6, Appli
45	465.5	34.8	436	4	US-10-200-910-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 93.9%; Score 1257; DB 4; Length 386;
Best Local Similarity 99.1%; Pred. No. 1.4e-131;
Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 120
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Db        175 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 234

Qy        121 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 180
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Qy        181 ELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
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RESULT 2
US-07-649-591B-3
; Sequence 3, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-649-591B-3

  Query Match             92.6%;  Score 1239.5;  DB 1;  Length 423;
  Best Local Similarity   86.2%;  Pred. No. 1.4e-129;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
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Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
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Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
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Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 3
US-08-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 5474901
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5474901el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,540
;      FILING DATE:  19-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-277-540-3

  Query Match             92.6%;  Score 1239.5;  DB 1;  Length 423;
  Best Local Similarity   86.2%;  Pred. No. 1.4e-129;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

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Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
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Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 4
US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-430-787A-3

  Query Match           92.6%;  Score 1239.5;  DB 1;  Length 423;
  Best Local Similarity   86.2%;  Pred. No. 1.4e-129;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 5
US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Plasma
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23..401
US-08-869-057-2

  Query Match           92.6%;  Score 1239.5;  DB 2;  Length 423;
  Best Local Similarity   86.2%;  Pred. No. 1.4e-129;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 6
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

  Query Match             91.8%;  Score 1228.5;  DB 4;  Length 423;
  Best Local Similarity   85.5%;  Pred. No. 2.4e-128;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 7
US-08-782-760-6
; Sequence 6, Application US/08782760
; Patent No. 5948668
;  GENERAL INFORMATION:
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Fulga, Netta
;    APPLICANT:  Mendelovitch, Simona
;    APPLICANT:  Gorecki, Marian
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/782,760
;      FILING DATE:  13-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/378,233
;      FILING DATE:  25-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-782-760-6

  Query Match             45.6%;  Score 610;  DB 2;  Length 307;
  Best Local Similarity   45.0%;  Pred. No. 1.6e-59;
  Matches  121;  Conservative   43;  Mismatches   65;  Indels   40;  Gaps    5;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||   | :|::   | :||: :   :||::|:  ||::||   :||||: || :  | ||
Db          1 ASGHSYTKYNNWETIEAWIQQVATDNPDLVTQSVIGTTFEGRNMYVLKI-GKTRPNKPAI 59

Qy         61 WIDCGIHAREWISPAFCLWFI-------------------------------GH------ 83
              :|||| ||||||||||| ||:                               |:
Db         60 FIDCGFHAREWISPAFCQWFVREAVRTYNQEIHMKQLLDELDFYVLPVVNIDGYVYTWTK 119

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              :||||| ||  | : |:| | |||| :  ||| ||| | |||||||  |||| | ||:|
Db        120 DRMWRKTRSTMAGSSCLGVDPNRNF-NAGWCEVGASRSPCSETYCGPAPESEKETKALAD 178

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              |:| |:: ||||:::|||||| :::|||||     :::|||: :   | : :  |   |:||
Db        179 FIRNNLSTIKAYLTIHSYSQMMLYPYSYDYKLPENYEELNALVKGAAKEL-ATLHGTKYT 237

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              :| |: |:| | || ||| || |||||||
Db        238 YGPGATTIYPAAGGSDDWSYDQGIKYSFT 266


RESULT 8
PCT-US96-00995-6
; Sequence 6, Application PC/TUS9600995
;  GENERAL INFORMATION:
;    APPLICANT:  Bio-Technology General Corp.
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00995
;      FILING DATE:  25-JAN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847-A-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 308 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-00995-6

  Query Match             45.6%;  Score 610;  DB 5;  Length 307;
  Best Local Similarity   45.0%;  Pred. No. 1.6e-59;
  Matches  121;  Conservative   43;  Mismatches   65;  Indels   40;  Gaps    5;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
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                ||    | :|::    | :||: :    :||::|:  ||::||   :||||: || :  | ||
Db          1 ASGHSYTKYNNWETIEAWIQQVATDNPDLVTQSVIGTTFEGRNMYVLKI-GKTRPNKPAI 59

Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
               :|||| ||||||||||| ||:                              |:
Db         60 FIDCGPHAREWISPAFCQWFVREAVRTYNQEIHMKQLLDELDFYVLPVVNIDGYVYTWTK 119

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               :||||| ||  | : |:| | |||| :  ||| ||| | |||||||  |||| | ||:|
Db        120 DRMWRKTRSTMAGSSCLGVDPNRNF-NAGWCEVGASRSPCSETYCGPAPESEKETKALAD 178

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               |:| |:: ||||:::|||| :::||||     :::|||: :   | : :  |   |:||
Db        179 FIRNNLSTIKAYLTIHSYSQMMLYPYSYDYKLPENYEELNALVKGAAKEL-ATLHGTKYT 237

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               :| |: |:| | || ||| || |||||||
Db        238 YGPGATTIYPAAGGSDDWSYDQGIKYSFT 266


RESULT 9
US-08-696-139-4
; Sequence 4, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  306 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-696-139-4

  Query Match           43.5%;  Score 582;  DB 1;  Length 306;
  Best Local Similarity  44.3%;  Pred. No. 2.2e-56;
  Matches  117;  Conservative   40;  Mismatches   67;  Indels   40;  Gaps    5;

Qy          6 YEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCG 65
```

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                ||:|::   | :| : :|  :||:::: ||::|    :|:||| ||    | ||::|||
Db          6 YEKYNNWETIEAWTKQVTSENPDLISRTAIGTTFLGNNIYLLKV-GKPGPNKPAIFMDCG 64

Qy         66 IHAREWISPAFCLWFI------------------------------GH------NRMWR 88
               ||||||| ||| ||:                              |:      |||||
Db         65 FHAREWISHAFCQWFVREAVLTYGYESHMTEFLNKLDFYVLPVLNIDGYIYTWTKNRMWR 124

Qy         89 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 148
               | ||  |   ||||| |||| |   ||  |||:  | |||||   ||| | ||:| |:| |
Db        125 KTRSTNAGTTCIGTDPNRNF-DAGWCTTGASTDPCDETYCGSAAESEKETKALADFIRNN 183

Qy        149 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 208
               :: ||||:::||||| |::|||| |   ::: ||: :|  ||: :  |   |:||:| |:
Db        184 LSSIKAYLTIHSYSQMILYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGA 242

Qy        209 ETLYLAPGGGDDWIYDLGIKYSFT 232
               |:| | || ||| || |||||||
Db        243 TTIYPAAGGSDDWAYDQGIKYSFT 266


RESULT 10
US-08-696-139-2
; Sequence 2, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  404 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-696-139-2

  Query Match           43.5%;  Score 582;  DB 1;  Length 404;
  Best Local Similarity  44.3%;  Pred. No. 3.3e-56;
  Matches  117;  Conservative   40;  Mismatches   67;  Indels   40;  Gaps    5;

Qy          6 YEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCG 65
```

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                ||:|::   | :| : :|  :||:::::  ||::|    :|:||| ||    | ||::|||
Db        104 YEKYNNWETIEAWTKQVTSENPDLISRTAIGTTFLGNNIYLLKV-GKPGPNKPAIFMDCG 162

Qy         66 IHAREWISPAFCLWFI------------------------------GH------NRMWR 88
               ||||||| ||| ||:                             |:      |||||
Db        163 FHAREWISHAFCQWFVREAVLTYGYESHMTEFLNKLDFYVLPVLNIDGYIYTWTKNRMWR 222

Qy         89 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 148
               | ||  |   ||||| ||||    ||  |||:  | |||||   ||| | ||:| |:| |
Db        223 KTRSTNAGTTCIGTDPNRNF-DAGWCTTGASTDPCDETYCGSAAESEKETKALADFIRNN 281

Qy        149 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 208
               :: ||||:::||||| |::|||     ::: ||: :|  ||: :  |   |:||:| |:
Db        282 LSSIKAYLTIHSYSQMILYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGA 340

Qy        209 ETLYLAPGGGDDWIYDLGIKYSFT 232
               |:| | || ||| || |||||||
Db        341 TTIYPAAGGSDDWAYDQGIKYSFT 364


RESULT 11
US-09-011-769A-51
; Sequence 51, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 51:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 329 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-011-769A-51

  Query Match             42.4%;  Score 567;  DB 4;  Length 329;
  Best Local Similarity   41.3%;  Pred. No. 1.1e-54;
  Matches  111;  Conservative   46;  Mismatches   72;  Indels   40;  Gaps    5;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
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Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
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Db         82 FMDCGFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTK 141

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               :| ||| || :  : ||||| ||||    ||| ||| : | |||||   ||| | ||:|
Db        142 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALAD 200

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               |:|  :: ||||:::||||| :::||||     ::: ||: :|   |: :  :   |:||
Db        201 FIRNKLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYT 259

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
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Db        260 YGPGATTIYPAAGGSDDWAYDQGIRYSFT 288


RESULT 12
US-09-011-769A-47
; Sequence 47, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 47:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 349 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-011-769A-47

  Query Match             42.4%;  Score 567;  DB 4;  Length 349;
  Best Local Similarity   41.3%;  Pred. No. 1.2e-54;
  Matches  111;  Conservative   46;  Mismatches   72;  Indels   40;  Gaps    5;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
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                |:   ||:|:    | :| : :   :| ::::  ||::||   :|:||| ||    | ||
Db         23 ATGHSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 81

Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
               ::||| ||||||||||| ||:                              |:
Db         82 FMDCGFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTK 141

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               :| ||| || :  : ||||| ||||    ||| ||| : | |||||   ||| | ||:|
Db        142 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALAD 200

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               |:|  :: ||||:::||||| :::||||     ::: ||: :|   |: :  :   |:||
Db        201 FIRNKLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYT 259

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               :| |: |:| | || ||| || ||:||||
Db        260 YGPGATTIYPAAGGSDDWAYDQGIRYSFT 288
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RESULT 13
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  415 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-860-882A-57

  Query Match           42.4%;  Score 567;  DB 2;  Length 415;
  Best Local Similarity   41.3%;  Pred. No. 1.6e-54;
  Matches  111;  Conservative   46;  Mismatches   72;  Indels   40;  Gaps    5;
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Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              |:   ||:|:    | :| : :   :| ::::  ||::||   :|:||| ||    | ||
Db        109 ATGHSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 167

Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
               ::||| ||||||||||| ||:                              |:
Db        168 FMDCGFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTK 227

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               :| ||| || :  : ||||| ||||    ||| ||| : | |||||   ||| | ||:|
Db        228 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALAD 286

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               |:|  :: ||||:::||||| :::||||     ::: ||: :|   |: :  :   |:||
Db        287 FIRNKLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYT 345

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               :| |: |:| | || ||| || ||:||||
Db        346 YGPGATTIYPAAGGSDDWAYDQGIRYSFT 374
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RESULT 14
US-09-011-769A-39
; Sequence 39, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;  INFORMATION FOR SEQ ID NO: 39:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 415 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39

  Query Match           42.4%;  Score 567;  DB 4;  Length 415;
  Best Local Similarity   41.3%;  Pred. No. 1.6e-54;
  Matches  111;  Conservative   46;  Mismatches   72;  Indels   40;  Gaps    5;
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Db        109 ATGHSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 167

Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
              ::||| |||||||||||| ||:                              |:
Db        168 FMDCGFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTK 227

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              :| ||| || :  : ||||| ||||    ||| ||| : | |||||   ||| | ||:|
Db        228 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALAD 286

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              |:|  :: ||||:::||||| :::||||     ::: ||: :|   |: :  :   |:||
Db        287 FIRNKLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYT 345

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
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Db        346 YGPGATTIYPAAGGSDDWAYDQGIRYSFT 374
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RESULT 15
US-09-011-769A-56
; Sequence 56, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 56:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 424 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-011-769A-56

  Query Match           42.4%;  Score 567;  DB 4;  Length 424;
  Best Local Similarity  41.3%;  Pred. No. 1.7e-54;
  Matches  111;  Conservative   46;  Mismatches   72;  Indels   40;  Gaps    5;
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Db        118 ATGHSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 176

Qy         61 WIDCGIHAREWISPAFCLWFI------------------------------GH------ 83
              ::||| |||||||||||| ||:                              |:
Db        177 FMDCGFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFYVLPVLNIDGYIYTWTK 236

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              :| ||| || :  : ||||| ||||    ||| ||| : | |||||   ||| | ||:|
Db        237 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAAESEKETKALAD 295

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              |:|  :: ||||:::||||| :::||||     ::: ||: :|   |: :  :   |:||
Db        296 FIRNKLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTKYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
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Db        355 YGPGATTIYPAAGGSDDWAYDQGIRYSFT 383
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Job time : 25.7627 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:43:44 ; Search time 56.2881 Seconds
(without alignments)
1416.943 Million cell updates/sec

Title: US-09-980-881A-4
Perfect score: 1338
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1257	93.9	386	14	US-10-212-877-2	Sequence 2, Appli
3	1239.5	92.6	423	14	US-10-379-836-17	Sequence 17, Appl
4	1228.5	91.8	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1228.5	91.8	423	14	US-10-212-877-4	Sequence 4, Appli
6	1216	90.9	428	15	US-10-115-479-68	Sequence 68, Appl
7	1216	90.9	428	15	US-10-115-479-70	Sequence 70, Appl
8	1164.5	87.0	423	14	US-10-379-836-2	Sequence 2, Appli
9	1105.5	82.6	422	14	US-10-379-836-18	Sequence 18, Appl
10	1095.5	81.9	422	14	US-10-379-836-16	Sequence 16, Appl
11	837	62.6	322	15	US-10-115-479-64	Sequence 64, Appl
12	816.5	61.0	211	9	US-09-925-302-467	Sequence 467, App
13	816.5	61.0	211	10	US-09-925-302-467	Sequence 467, App
14	798	59.6	354	15	US-10-115-479-66	Sequence 66, Appl
15	582	43.5	416	15	US-10-074-978A-269	Sequence 269, App
16	578	43.2	416	15	US-10-074-978A-270	Sequence 270, App
17	567	42.4	402	14	US-10-379-836-20	Sequence 20, Appl
18	567	42.4	417	15	US-10-074-978A-267	Sequence 267, App
19	567	42.4	417	15	US-10-074-978A-268	Sequence 268, App
20	567	42.4	417	16	US-10-477-515-3	Sequence 3, Appli
21	552	41.3	417	14	US-10-229-546-2	Sequence 2, Appli
22	552	41.3	417	14	US-10-229-546-9	Sequence 9, Appli
23	552	41.3	417	14	US-10-341-434-188	Sequence 188, App
24	552	41.3	417	15	US-10-262-511-72	Sequence 72, Appl
25	550.5	41.1	374	9	US-09-888-615-61	Sequence 61, Appl
26	550.5	41.1	444	14	US-10-176-306-74	Sequence 74, Appl
27	549	41.0	434	16	US-10-477-515-2	Sequence 2, Appli
28	549	41.0	437	13	US-10-200-344-10	Sequence 10, Appl
29	549	41.0	437	14	US-10-274-639-12	Sequence 12, Appl
30	549	41.0	437	15	US-10-333-574-12	Sequence 12, Appl
31	549	41.0	613	9	US-09-910-059-113	Sequence 113, App
32	549	41.0	613	16	US-10-608-710-4	Sequence 4, Appli
33	549	41.0	716	9	US-09-910-059-125	Sequence 125, App
34	547.5	40.9	416	15	US-10-074-978A-266	Sequence 266, App
35	547	40.9	437	17	US-10-757-262-128	Sequence 128, App
36	530	39.6	286	15	US-10-072-012-887	Sequence 887, App
37	519	38.8	286	16	US-10-408-765A-1959	Sequence 1959, Ap
38	502.5	37.6	419	15	US-10-072-012-788	Sequence 788, App
39	501.5	37.5	298	14	US-10-379-836-19	Sequence 19, Appl
40	492	36.8	399	14	US-10-200-910-8	Sequence 8, Appli
41	492	36.8	399	17	US-10-843-130-8	Sequence 8, Appli
42	488.5	36.5	419	15	US-10-072-012-787	Sequence 787, App
43	471.5	35.2	350	13	US-10-200-344-12	Sequence 12, Appl
44	465.5	34.8	406	9	US-09-925-297-517	Sequence 517, App
45	465.5	34.8	419	14	US-10-345-680-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 93.9%; Score 1257; DB 9; Length 386;
Best Local Similarity 99.1%; Pred. No. 5.1e-121;
Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 234

Qy        121 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 294
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Qy        181 ELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        295 ELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 2
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-212-877-2

  Query Match             93.9%;  Score 1257;  DB 14;  Length 386;
  Best Local Similarity   99.1%;  Pred. No. 5.1e-121;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 234

Qy        121 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 294

Qy        181 ELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        295 ELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 346


RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-836-17

  Query Match             92.6%;  Score 1239.5;  DB 14;  Length 423;
  Best Local Similarity   86.2%;  Pred. No. 3.7e-119;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173
;  CURRENT APPLICATION NUMBER: US/09/813,133A
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Human
US-09-813-133A-4

  Query Match             91.8%;  Score 1228.5;  DB 9;  Length 423;
  Best Local Similarity   85.5%;  Pred. No. 5.1e-118;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
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;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;    LENGTH: 423
;    TYPE: PRT
;    ORGANISM: Human
US-10-212-877-4

  Query Match             91.8%;  Score 1228.5;  DB 14;  Length 423;
  Best Local Similarity   85.5%;  Pred. No. 5.1e-118;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        295 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISKNTRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||
Db        355 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 383


RESULT 6
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No.. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li,. Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-115-479-68

  Query Match             90.9%;  Score 1216;  DB 15;  Length 428;
  Best Local Similarity   83.9%;  Pred. No. 1e-116;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels   42;  Gaps    2;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQT 55
              |||||||||||||||||||||||||||||||||||||||||||||||||     ||||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQA 174

Qy         56 AKNAIWIDCGIHAREWISPAFCLWFIGH------------------------------ 83
              ||||||||||||||||||||||||||||
Db        175 AKNAIWIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYD 234

Qy         84 -----NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEV 138
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 YSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEV 294

Qy        139 KAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSK 198
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        295 KAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISK 354

Qy        199 NTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              |||||||||||||||||||||||||||||||||
Db        355 NTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 388


RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
```

```
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-70

  Query Match             90.9%;  Score 1216;  DB 15;  Length 428;
  Best Local Similarity   83.9%;  Pred. No. 1e-116;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels   42;  Gaps    2;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQT 55
              ||||||||||||||||||||||||||||||||||||||||||||||||     ||||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQA 174

Qy         56 AKNAIWIDCGIHAREWISPAFCLWFIGH-------------------------------- 83
              ||||||||||||||||||||||||||||
Db        175 AKNAIWIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYD 234

Qy         84 -----NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEV 138
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 YSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEV 294

Qy        139 KAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSK 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        295 KAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISK 354

Qy        199 NTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||||||
Db        355 NTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 388


RESULT 8
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Papio hamadryas
US-10-379-836-2

  Query Match             87.0%;  Score 1164.5;  DB 14;  Length 423;
  Best Local Similarity   80.7%;  Pred. No. 2.1e-111;
  Matches  217;  Conservative    7;  Mismatches    8;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              |||||||||||||||||||| |||::|||||||||||:||:|||||||||||||||||:
Db        115 ASASYYEQYHSLNEIYSWIELITEKYPDMLTKIHIGSSYEKHPLYVLKVSGKEQTAKNAM 174

Qy         61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
              |||||||||||||||||||||||
Db        175 WIDCGIHAREWISPAFCLWFIGHITEYYGIIGEYTNLLRHVDFYVMPVVNVDGYDYSWKK 234

Qy         84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
              ||||||||||||||| |||||||||||||||||||| |||||||||||||||| ||||:
Db        235 NRMWRKNRSFYANNRCIGTDLNRNFASKHWCEEGASSFSCSETYCGLYPESEPEAKAVAN 294

Qy        144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
              ||||||| |||||||||||||||||||||||||||||||||||||:||||| |||
Db        295 FLRRNINHIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIQKTSKNIRYT 354

Qy        204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              || |||||||||| ||||||||||||||
Db        355 HGRGSETLYLAPGGADDWIYDLGIKYSFT 383


RESULT 9
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-379-836-18

  Query Match             82.6%;  Score 1105.5;  DB 14;  Length 422;
  Best Local Similarity   77.0%;  Pred. No. 2.6e-105;
  Matches  207;  Conservative   10;  Mismatches   15;  Indels   37;  Gaps    1;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
              |||||||||||||||||||| |||:|||||| ||:|||||||||||||||||  ||||
Db        114 ASASYYEQYHSLNEIYSWIEVITEQHPDMLQKIYIGSSFEKYPLYVLKVSGKEQRIKNAI 173
```

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Qy          61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
               |||||||||||||||||||||||:
Db         174 WIDCGIHAREWISPAFCLWFIGYVTQFHGKENLYTRLLRHVDFYIMPVMNVDGYDYTWKK 233

Qy          84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               ||||||||| : || |:||||||||||||||:||||||||||||||||||||||||||
Db         234 NRMWRKNRSAHKNNRCVGTDLNRNFASKHWCEKGASSSSCSETYCGLYPESEPEVKAVAD 293

Qy         144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               ||||||: |||||||||||| |:||||| ||||||||||||||||||  :||||||
Db         294 FLRRNIDHIKAYISMHSYSQQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYT 353

Qy         204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               || |||:||||||| ||||||||||||||
Db         354 HGSGSESLYLAPGGSDDWIYDLGIKYSFT 382


RESULT 10
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-379-836-16

  Query Match           81.9%;  Score 1095.5;  DB 14;  Length 422;
  Best Local Similarity   75.8%;  Pred. No. 2.8e-104;
  Matches  204;  Conservative   11;  Mismatches   17;  Indels   37;  Gaps    1;

Qy           1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
               ||:||||||||||||||| |||:||||| ||:||||:|||||||||||||   ||||
Db         114 ASSSYYEQYHSLNEIYSWIEVITEQHPDMLQKIYIGSSYEKYPLYVLKVSGKEHRVKNAI 173

Qy          61 WIDCGIHAREWISPAFCLWFIGH---------------------------------- 83
               |||||||||||||||||||||||:
Db         174 WIDCGIHAREWISPAFCLWFIGYVTQFHGKENTYTRLLRHVDFYIMPVMNVDGYDYTWKK 233

Qy          84 NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVAS 143
               ||||||||| : || |:||||||||||||||:|||| ||||||||||||||||||||
Db         234 NRMWRKNRSVHMNNRCVGTDLNRNFASKHWCEKGASSFSCSETYCGLYPESEPEVKAVAD 293

Qy         144 FLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
               ||||||| |||||||||||| |:||||| ||||||||||||||||||||  :||||||
Db         294 FLRRNINHIKAYISMHSYSQQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYT 353

Qy         204 HGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               || |||:||||||| ||||||||||||||
Db         354 HGSGSESLYLAPGGSDDWIYDLGIKYSFT 382


RESULT 11
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-64

  Query Match           62.6%;  Score 837;  DB 15;  Length 322;
  Best Local Similarity   71.6%;  Pred. No. 1e-77;
  Matches  166;  Conservative    0;  Mismatches    2;  Indels   64;  Gaps    1;

Qy           1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAI 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db         115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQAAKNAI 174

Qy          61 WIDCGIHAREWISPAFCLWFIGHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASS 120
               |||
Db         175 WID---------------------------------------------------------- 177

Qy         121 SSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 180
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 -------CGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHE 230

Qy         181 ELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
               |||||||||||||| |||||||||||||||||||||||||||||||||||||
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Db        231 ELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 282


RESULT 12
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

  Query Match           61.0%;  Score 816.5;  DB 9;  Length 211;
  Best Local Similarity   90.6%;  Pred. No. 7.6e-76;
  Matches  154;  Conservative    1;  Mismatches    6;  Indels    9;  Gaps    2;

Qy         71 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 122
              |||   | | :         ||||||||||||||||||||||||||||||||||||||
Db          3 WIS-MLCRWLMWMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 61

Qy        123 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        183 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-302-467

  Query Match           61.0%;  Score 816.5;  DB 10;  Length 211;
  Best Local Similarity   90.6%;  Pred. No. 7.6e-76;
  Matches  154;  Conservative    1;  Mismatches    6;  Indels    9;  Gaps    2;

Qy         71 WISPAFCLWFI--------GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 122
              |||   | | :         ||||||||||||||||||||||||||||||||||||||
Db          3 WIS-MLCRWLMWMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSS 61

Qy        123 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        183 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171


RESULT 14
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PC)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-479-66

  Query Match           59.6%;  Score 798;  DB 15;  Length 354;
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```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Qy        183 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 171
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  Best Local Similarity   57.3%;  Pred. No. 1.3e-73;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels  116;  Gaps    3;

Qy          1 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLK-----VSGKEQT 55
              ||||||||||||||||||||||||||||||||||||||||||||||||     ||||||
Db        115 ASASYYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKGFFEQVSGKEQA 174

Qy         56 AKNAIWIDCGIHAREWISPAFCLWFIGH------------------------------ 83
              ||||||||||||||||||||||||||||
Db        175 AKNAIWIDCGIHAREWISPAFCLWFIGHITQFYGIIGQYTNLLRLVDFYVMPVVNVDGYD 234

Qy         84 -----NRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEV 138
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 YSWKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPE----- 289

Qy        139 KAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSK 198

Db        290 ------------------------------------------------------------ 289

Qy        199 NTRYTHGHGSETLYLAPGGGDDWIYDLGIKYSFT 232
                     |||||||||||||||||||||||||
Db        290 ---------SETLYLAPGGGDDWIYDLGIKYSFT 314


RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;  APPLICANT: Leite, Mario
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Li, Li
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Liu, Xiahong
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Blalock, Angela
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter S
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Heyes, Melvin P
;  APPLICANT:  Herrman, John
;  APPLICANT:  Pena, Carol E A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Moore, No. US20040010119A1lle
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Stone, Dave
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Peyman, John
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-269
;  CURRENT APPLICATION NUMBER: US/10/074,978A
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/268,221
;  PRIOR FILING DATE: 2001-02-12
;  PRIOR APPLICATION NUMBER: 60/335,109
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 60/312,284
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: 60/268,496
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/276,703
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/330,293
;  PRIOR FILING DATE: 2001-10-18
;  PRIOR APPLICATION NUMBER: 60/322,127
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/280,899
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/310,797
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/268,646
;  PRIOR FILING DATE: 2001-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-10-074-978A-269

  Query Match            43.5%;  Score 582;  DB 15;  Length 416;
  Best Local Similarity  44.3%;  Pred. No. 3.3e-51;
  Matches  117;  Conservative   40;  Mismatches   67;  Indels   40;  Gaps    5;

Qy          6 YEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSGKEQTAKNAIWIDCG 65
              ||:|::   | :| : :|  :||:::  ||::|    :|:||| ||    | ||::|||
Db        116 YEKYNNWETIEAWTKQVTSENPDLISRTAIGTTFLGNNIYLLKV-GKPGPNKPAIFMDCG 174

Qy         66 IHAREWISPAFCLWFI------------------------------GH------NRMWR 88
               ||||||| ||| ||:                              |:      |||||
Db        175 FHAREWISHAFCQWFVREAVLTYGYESHMTEFLNKLDFYVLPVLNIDGYIYTWTKNRMWR 234

Qy         89 KNRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 148
              | ||  |   ||||| ||||    ||  |||:  | |||||   ||| | ||:| |:| |
Db        235 KTRSTNAGTTCIGTDPNRNF-DAGWCTTGASTDPCDETYCGSAAESEKETKALADFIRNN 293

Qy        149 INQIKAYISMHSYSQHIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 208
              :: ||||:::||||| |::|||     ::: ||: :|  ||: :  |   |:||:| |:
Db        294 LSSIKAYLTIHSYSQMILYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTKYTYGPGA 352

Qy        209 ETLYLAPGGGDDWIYDLGIKYSFT 232
               |:| | || ||| || |||||||
Db        353 TTIYPAAGGSDDWAYDQGIKYSFT 376


Search completed: October 28, 2004, 20:05:52
Job time : 57.2881 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 03:40:54 ; Search time 71.6631 Seconds
(without alignments)
2439.944 Million cell updates/sec

Title: US-09-980-881A-4
Perfect score: 1338
Sequence: 1 ASASYYEQYHSLNEIYSWIE.....IKYSFTSNPPVEKLLPLSLK 246

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1289.5	96.4	1625	4	US-09-813-133A-1	Sequence 1, Appli
2	1272	95.1	1272	2	US-08-869-057-1	Sequence 1, Appli
3	1272	95.1	1749	1	US-07-649-591B-2	Sequence 2, Appli
4	1272	95.1	1749	1	US-08-277-540-2	Sequence 2, Appli
5	1272	95.1	1749	1	US-08-430-787A-2	Sequence 2, Appli
6	610	45.6	927	2	US-08-782-760-5	Sequence 5, Appli
7	610	45.6	927	5	PCT-US96-00995-5	Sequence 5, Appli
8	582	43.5	921	1	US-08-696-139-3	Sequence 3, Appli
9	582	43.5	1215	1	US-08-696-139-1	Sequence 1, Appli
10	567	42.4	999	2	US-08-860-882A-67	Sequence 67, Appl
11	567	42.4	999	4	US-09-011-769A-50	Sequence 50, Appl
12	567	42.4	1053	2	US-08-860-882A-64	Sequence 64, Appl
13	567	42.4	1053	4	US-09-011-769A-46	Sequence 46, Appl
14	567	42.4	1263	2	US-08-860-882A-56	Sequence 56, Appl
15	567	42.4	1263	4	US-09-011-769A-38	Sequence 38, Appl
16	567	42.4	1284	2	US-08-860-882A-71	Sequence 71, Appl
17	567	42.4	1284	4	US-09-011-769A-55	Sequence 55, Appl
18	560	41.9	1053	4	US-09-463-451-27	Sequence 27, Appl
c 19	560	41.9	1053	4	US-09-463-451-28	Sequence 28, Appl
20	560	41.9	1059	2	US-08-860-882A-74	Sequence 74, Appl
21	560	41.9	1059	4	US-09-011-769A-59	Sequence 59, Appl
22	559	41.8	1059	2	US-08-860-882A-77	Sequence 77, Appl
23	559	41.8	1059	4	US-09-011-769A-63	Sequence 63, Appl
24	556.5	41.6	1311	4	US-09-675-305-9	Sequence 9, Appli
25	556.5	41.6	1311	4	US-10-200-344-9	Sequence 9, Appli
26	552	41.3	1622	4	US-09-023-655-1020	Sequence 1020, Ap
27	549	41.0	1870	3	US-09-171-945-112	Sequence 112, App
28	549	41.0	2154	3	US-09-171-945-124	Sequence 124, App
29	525.5	39.3	2128	4	US-09-675-305-13	Sequence 13, Appl
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31	492	36.8	1200	4	US-09-710-099-7	Sequence 7, Appli
32	492	36.8	1200	4	US-10-200-910-7	Sequence 7, Appli
33	471.5	35.2	1050	4	US-09-675-305-11	Sequence 11, Appl
34	471.5	35.2	1050	4	US-10-200-344-11	Sequence 11, Appl
35	465.5	34.8	1257	3	US-08-640-906-1	Sequence 1, Appli
36	465.5	34.8	1257	3	US-09-395-936-1	Sequence 1, Appli
37	465.5	34.8	1311	4	US-09-710-099-5	Sequence 5, Appli
38	465.5	34.8	1311	4	US-10-200-910-5	Sequence 5, Appli
39	459	34.3	1251	3	US-08-640-906-3	Sequence 3, Appli
40	459	34.3	1251	3	US-09-395-936-3	Sequence 3, Appli
41	405.5	30.3	945	4	US-09-710-099-3	Sequence 3, Appli
42	405.5	30.3	945	4	US-09-710-099-11	Sequence 11, Appl
43	405.5	30.3	945	4	US-10-200-910-3	Sequence 3, Appli
44	405.5	30.3	945	4	US-10-200-910-11	Sequence 11, Appl
45	403.5	30.2	2247	4	US-09-710-099-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

Pred. No.:	3.46e-156	Length:	1625
Score:	1289.50	Matches:	244
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Best Local Similarity:	92.42%	Mismatches:	2
Query Match:	96.38%	Indels:	18
DB:	4	Gaps:	1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

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Db        359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 418

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        419 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 478

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        479 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATA 538

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 598

Qy         81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATC 658

Qy        101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGT 718

Qy        121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 TCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCA 778

Qy        141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
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Db        779 GTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCA 838

Qy        161 TyrSerGlnHisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 TACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAG 898

Qy        181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        899 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACC 958

Qy        201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
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Db        959 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGAT 1018

Qy        221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe-------------------------- 231
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Db       1019 TGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACA 1078

Qy        232 ------------------------ThrSerAsnProProValGluLysLeuLeuProLe 243
                                       ||||||||||||||||||||||||||||||||||
Db       1079 TACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCT 1138

Qy        243 uSerLeuLys 246
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Db       1139 GTCTCTAAAA 1148

RESULT 2
US-08-869-057-1
; Sequence 1, Application US/08869057
; Patent No. 5985562
;  GENERAL INFORMATION:
;    APPLICANT:  Morser, Michael J
;    APPLICANT:  Nagashima, Mariko
;    TITLE OF INVENTION:  Method of Detecting Thrombotic Disease
;    TITLE OF INVENTION:  Risk
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Berlex Biosciences Legal Department
;      STREET:  15049 San Pablo Avenue
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94804-0099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/869,057
;      FILING DATE:  03-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Washtien, Wendy L
;      REGISTRATION NUMBER:  36,301
;      REFERENCE/DOCKET NUMBER:  51509AUSM1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-262-5411
;      TELEFAX:  510-262-7095
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    PUBLICATION INFORMATION:
;      AUTHORS:  Eaton, Dan L.
;      AUTHORS:  Malloy, Beth E.
;      AUTHORS:  Tsai, Siao P
;      AUTHORS:  Henzel, William
;      AUTHORS:  Drayna, Dennis
;      TITLE:  Isolation, Molecular Cloning, and Partial
;      TITLE:  Characterization of a No. 5985562el Carboxypeptidase B
;      TITLE:  from Human Plasma
;      JOURNAL:  J. Biol. Chem.
;      VOLUME:  266
;      ISSUE:  32
;      PAGES:  21833-21838
;      DATE:  No. 5985562 15-1991
US-08-869-057-1

Alignment Scores:
Pred. No.:                4.21e-154      Length:          1272
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Best Local Similarity:    81.73%         Mismatches:      0
Query Match:              95.07%         Indels:          55
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US-09-980-881A-4 (1-246) x US-08-869-057-1 (1-1272)

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Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
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Db        463 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATA 522

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
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Qy         81 IleGlyHis---------------------------------------------------- 83
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Qy         83 ------------------------------------------------------------ 83

Db        643 GTGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 702

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGAC 762

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
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Db        763 CTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 822

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
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Db        823 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGT 882

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
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Db        883 TTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAG 942

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
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Db        943 CATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCT 1002

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
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Db       1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACA 1062

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
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Db       1063 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTAT 1122

Qy        224 AspLeuGlyIleLysTyrSerPhe---------------------------------- 231
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Db       1123 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTC 1182

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                               ||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTGCCGCTGTCTCTAAA 1242

Qy        246 s 246
              |
Db       1243 A 1243

RESULT 3
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis Drayna and Daniel Eaton
;    TITLE OF INVENTION:  No. 5206161el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/649,591B
;      FILING DATE:  19910201
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  hybridization probe
;      LOCATION:  133 to 178
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  potential clip site
;      LOCATION:  380 to 382
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  signal sequence
;      LOCATION:  41 to 106
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-07-649-591B-2

Alignment Scores:
Pred. No.:              7.12e-154      Length:          1749
Score:                  1272.00        Matches:         246
Percent Similarity:     81.73%         Conservative:    0
Best Local Similarity:  81.73%         Mismatches:      0
Query Match:            95.07%         Indels:          55
DB:                     1              Gaps:            2

US-09-980-881A-4 (1-246) x US-07-649-591B-2 (1-1749)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
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Db        383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 442

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 502

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATA 562

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 622

Qy         81 IleGlyHis---------------------------------------------------- 83
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Db        623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTT 682

Qy         83 ---------------------------------------------------------- 83

Db        683 GTGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 742

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
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Db        743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGAC 802

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 CTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGT 922

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
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Db        923 TTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAG 982

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
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Db        983 CATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCT 1042
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Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
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Db       1043 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACA 1102

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
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Db       1103 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTAT 1162

Qy        224 AspLeuGlyIleLysTyrSerPhe---------------------------------- 231
              |||||||||||||||||||||||
Db       1163 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTC 1222

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                               ||||||||||||||||||||||||||||||||||||||||||||
Db       1223 TTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAA 1282

Qy        246 s 246
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Db       1283 A 1283
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RESULT 4
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-277-540-2

Alignment Scores:

Pred. No.:	7.12e-154	Length:	1749
Score:	1272.00	Matches:	246
Percent Similarity:	81.73%	Conservative:	0
Best Local Similarity:	81.73%	Mismatches:	0
Query Match:	95.07%	Indels:	55
DB:	1	Gaps:	2

US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)

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Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 442

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 502

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATA 562

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 622

Qy         81 IleGlyHis---------------------------------------------------- 83
              |||||||||
Db        623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTT 682

Qy         83 ---------------------------------------------------------- 83

Db        683 GTGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 742

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGAC 802

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 CTGAATAGGAACTTTGCTTCCAAACACTCGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGT 922

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 TTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAG 982

Qy        164 HisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 CATATAGTGTTTCCATATTCCTATACACCAAGTAAAAGCAAAGACCATGAGGAACTGTCT 1042

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACA 1102

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTAT 1162

Qy        224 AspLeuGlyIleLysTyrSerPhe---------------------------------- 231
              |||||||||||||||||||||||
Db       1163 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTC 1222

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                               ||||||||||||||||||||||||||||||||||||||||||||
Db       1223 TTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAA 1282

Qy        246 s 246
              |
Db       1283 A 1283
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RESULT 5
US-08-430-787A-2
; Sequence 2, Application US/08430787A

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; Patent No. 5593674
;  GENERAL INFORMATION:
;    APPLICANT:  Drayna, Dennis T., Eaton, Dan L.
;    TITLE OF INVENTION:  No. 5593674el Plasma Carboxypeptidase
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,787A
;      FILING DATE:  27-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,540
;      FILING DATE:  19-JUL-1994
;      APPLICATION NUMBER:  08/167727
;      FILING DATE:  15-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/959944
;      FILING DATE:  14-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/649591
;      FILING DATE:  01-FEB-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  689D1C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1749 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-787A-2

Alignment Scores:
Pred. No.:              7.12e-154       Length:         1749
Score:                  1272.00         Matches:        246
Percent Similarity:     81.73%          Conservative:   0
Best Local Similarity:  81.73%          Mismatches:     0
Query Match:            95.07%          Indels:         55
DB:                     1               Gaps:           2

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 442

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 502

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATA 562

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 622

Qy         81 IleGlyHis---------------------------------------------------- 83
              |||||||||
Db        623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTT 682

Qy         83 ---------------------------------------------------------- 83

Db        683 GTGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 742

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGAC 802

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 CTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGT 922

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 TTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAG 982

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 CATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCT 1042

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACA 1102

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTAT 1162

Qy        224 AspLeuGlyIleLysTyrSerPhe------------------------------------ 231
              |||||||||||||||||||||||
Db       1163 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTC 1222

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                               ||||||||||||||||||||||||||||||||||||||||||||
Db       1223 TTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAA 1282

Qy        246 s 246
              |
Db       1283 A 1283

RESULT 6
US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
;  GENERAL INFORMATION:
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Fulga, Netta
;    APPLICANT:  Mendelovitch, Simona
;    APPLICANT:  Gorecki, Marian
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/782,760
;      FILING DATE:  13-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/378,233
;      FILING DATE:  25-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  927 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..927
US-08-782-760-5

Alignment Scores:
Pred. No.:              8.48e-69      Length:         927
Score:                  610.00        Matches:        126
Percent Similarity:     60.50%        Conservative:   44
Best Local Similarity:  44.84%        Mismatches:     71
Query Match:            45.59%        Indels:         41
DB:                     2             Gaps:           5

US-09-980-881A-4 (1-246) x US-08-782-760-5 (1-927)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||         |||   :::|||:::::::         |||   :::||||||:::
Db          1 GCAAGTGGACACAGCTACACCAAGTACAACAACTGGGAAACGATTGAGGCGTGGATTCAA 60

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::       :::||||||::::::|||:::       ||||||::::::||||||
Db         61 CAAGTTGCCACTGATAATCCAGACCTTGTCACTCAGAGCGTCATTGGAACCACATTTGAA 120

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||||||||||:::   ||||||   :::       |||   ||||||
Db        121 GGACGTAACATGTATGTCCTCAAGATT---GGTAAAACTAGACCGAATAAGCCTGCCATC 177

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              :::||||||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTTCTCCTGCATTCTGTCAGTGGTTT 237

Qy         81 Ile---------------------------------------------------------- 81
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Db        238 GTGAGAGAGGCTGTCCGTACCTATAATCAAGAGATCCACATGAAACAGCTTCTAGATGAA 297

Qy         82 ----------------------------------GlyHis------------------ 83
                                                |||:::
Db        298 CTGGATTTCTATGTTCTGCCTGTGGTCAACATTGATGGCTATGTCTACACCTGGACTAAG 357

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::||||||||||||||||   ||||||      |||   :::   |||:::|||   |||
Db        358 GACAGAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGAC 417

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
                 ||||||||||||   :::      |||||||||   |||||||||   |||   |||
Db        418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||      ||||||||||||   |||   ||||||:::|||
Db        475 TCTGAAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||   |||::::::   ||||||||||||:::::::::||||||||||||||||
Db        535 TTCATCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAG 594

Qy        164 HisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
                 :::::::::|||||||||||||                :::::::::|||||||||:::
Db        595 ATGATGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
                 :::          |||   :::   :::       |||          |||:::||||||
Db        655 GCCCTGGTGAAAGGTGCGGCAAAGGAGCCT---GCCACTCTGCATGGCACCAAGTACACA 711

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
                 :::|||   |||:::   |||:::|||   |||   ||||||   ||||||||   |||
Db        712 TATGGCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTAT 771

Qy        224 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 243
                 |||   ||||||||||||||||||||||          |||       :::||||||   |||
Db        772 GATCAGGGAATCAAATATTCCTTTACCTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830

Qy        244 Ser 244
                 |||
Db        831 TCT 833

RESULT 7
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
;  GENERAL INFORMATION:
;    APPLICANT:  Bio-Technology General Corp.
;    TITLE OF INVENTION:  PRODUCTION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00995
;      FILING DATE:  25-JAN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0336/43847-A-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  927 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..927
PCT-US96-00995-5

Alignment Scores:
Pred. No.:              8.48e-69      Length:         927
Score:                  610.00        Matches:        126
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Percent Similarity:     60.50%          Conservative:  44
Best Local Similarity:  44.84%          Mismatches:    71
Query Match:            45.59%          Indels:        41
DB:                     5               Gaps:          5

US-09-980-881A-4 (1-246) x PCT-US96-00995-5 (1-927)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||          |||   :::|||::::::          |||   :::||||||:::
Db          1 GCAAGTGGACACAGCTACACCAAGTACAACAACTGGGAAACGATTGAGGCGTGGATTCAA 60

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              :::         :::|||||::::::|||:::      ||||||::::::||||||
Db         61 CAAGTTGCCACTGATAATCCAGACCTTGTCACTCAGAGCGTCATTGGAACCACATTTGAA 120

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::||||||||||||:::   ||||||   :::      |||   ||||||
Db        121 GGACGTAACATGTATGTCCTCAAGATT---GGTAAAACTAGACCGAATAAGCCTGCCATC 177

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              :::||||||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTTCTCCTGCATTCTGTCAGTGGTTT 237

Qy         81 Ile------------------------------------------------------- 81
              :::
Db        238 GTGAGAGAGGCTGTCCGTACCTATAATCAAGAGATCCACATGAAACAGCTTCTAGATGAA 297

Qy         82 ---------------------------------GlyHis------------------ 83
                                                  |||:::
Db        298 CTGGATTTCTATGTTCTGCCTGTGGTCAACATTGATGGCTATGTCTACACCTGGACTAAG 357

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::||||||||||||||   ||||||      |||   :::   |||:::|||   |||
Db        358 GACAGAATGTGGAGAAAAACCCGCTCTACTATGGCTGGAAGTTCCTGCTTGGGTGTAGAC 417

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||   :::      |||||||||   |||||||||   |||   |||
Db        418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||      ||||||||||||   |||   ||||||:::|||
Db        475 TCTGAAACTTACTGTGGACCAGCCCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||   |||::::::   ||||||||||||:::::::::||||||||||||||
Db        535 TTCATCCGCAACAACCTCTCCACCATCAAGGCCTACCTGACCATCCACTCATACTCACAG 594

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::||||||||||||          :::::::::|||||||||:::
Db        595 ATGATGCTCTACCCTTACTCCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::         |||   :::   :::      |||         |||:::||||||
Db        655 GCCCTGGTGAAAGGTGCGGCAAAGGAGCTT---GCCACTCTGCATGGCACCAAGTACACA 711

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   ||||||||   |||
Db        712 TATGGCCCAGGAGCTACAACAATCTATCCTGCTGCTGGGGGATCTGACGACTGGTCTTAT 771

Qy        224 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 243
              |||   ||||||||||||||||||||          |||       :::||||||   |||
Db        772 GATCAGGGAATCAAATATTCCTTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830

Qy        244 Ser 244
              |||
Db        831 TCT 833

RESULT 8
US-08-696-139-3
; Sequence 3, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..921
US-08-696-139-3

Alignment Scores:
Pred. No.:              3.48e-65        Length:        921
Score:                  582.00          Matches:       117
Percent Similarity:     59.47%          Conservative:  40
Best Local Similarity:  44.32%          Mismatches:    67
Query Match:            43.50%          Indels:        40
DB:                     1               Gaps:          5

US-09-980-881A-4 (1-246) x US-08-696-139-3 (1-921)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||:::|||::::::          |||   :::|||   :::   :::|||
Db         16 TATGAGAAGTACAACAACTGGGAAACGATCGAGGCTTGGACTAAGCAAGTCACCAGTGAA 75

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              :::||||||:::::::::::      ||||||::::::|||            :::|||
Db         76 AATCCAGACCTCATCTCTCGCACAGCCATCGGAACTACATTTTTAGGAAACAATATATAC 135

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::||||||||||   ||||||            |||   ||||||::::::||||||||
Db        136 CTCCTCAAGGTT---GGCAAACCTGGACCAAATAAGCCTGCCATTTTCATGGACTGTGGT 192

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81
                 ||||||||||||||||||||   |||||||||   ||||||:::
Db        193 TTCCATGCCAGAGAATGGATTTCCCATGCATTTTGCCAGTGGTTTGTGAGAGAGGCTGTT 252

Qy         81 ------------------------------------------------------------ 81
```

```
Db        253 CTCACCTATGGATATGAGAGTCACATGACAGAATTCCTCAACAAGCTAGACTTTTATGTC 312

Qy         82 ----------------------GlyHis------------------AsnArgMetTrpArg 88
                                    |||:::                 ||||||||||||||
Db        313 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGA 372

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
              |||   ||||||      |||          ||||||||||||||   ||||||||||||
Db        373 AAGACCCGCTCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTT 432

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
                  ||||||      |||||||||:::      |||   ||||||||||||
Db        433 ---GATGCTGGGTGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGT 489

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
              |||         |||||||||   |||   ||||||:::|||   |||:::|||   |||
Db        490 GGATCTGCTGCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAAC 549

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
              ::::::   ||||||||||||:::::::::|||||||||||||||||   |||::::::|||
Db        550 CTCTCCTCCATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCT 609

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||                 :::::::::   ||||||:::   :::|||
Db        610 TATTCCTATGATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCT 669

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
              ||||||:::   :::      |||         |||:::||||||:::|||   |||:::
Db        670 GCCGTGAAAGAACTT---GCTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCT 726

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
              |||:::|||   |||   ||||||   |||||||||   ||||||   ||||||||||
Db        727 ACAACAATCTATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAA 786

Qy        229 TyrSerPheThr 232
              ||||||||||||
Db        787 TATTCCTTCACC 798
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```
RESULT 9
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
;  GENERAL INFORMATION:
;    APPLICANT:  Fayerman, Jeffrey T.
;    APPLICANT:  Greenen, David P.
;    APPLICANT:  Hershberger, Charles L.
;    APPLICANT:  Larson, Jeffrey L.
;    APPLICANT:  Sterner, Jane L.
;    APPLICANT:  Zhang, Haichao
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PORCINE
;    TITLE OF INVENTION:  PANCREATIC CARBOXYPEPTIDASE B
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,139
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,258
;      FILING DATE:  16-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-8681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1215 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1215
US-08-696-139-1

Alignment Scores:
Pred. No.:                5.49e-65      Length:          1215
Score:                    582.00        Matches:         117
Percent Similarity:       59.47%        Conservative:    40
Best Local Similarity:    44.32%        Mismatches:      67
Query Match:              43.50%        Indels:          40
DB:                       1             Gaps:            5

US-09-980-881A-4 (1-246) x US-08-696-139-1 (1-1215)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||:::|||::::::          |||   :::|||   :::   :::|||
Db        310 TATGAGAAGTACAACAACTGGGAAACGATCGAGGCTTGGACTAAGCAAGTCACCAGTGAA 369

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              :::||||||:::::::::::       ||||||:::::|||            :::|||
Db        370 AATCCAGACCTCATCTCTCGCACAGCCATCGGAACTACATTTTTAGGAAACAATATATAC 429

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::||||||||||   ||||||          |||   ||||||::::::||||||||
Db        430 CTCCTCAAGGTT---GGCAAACCTGGACCAAATAAGCCTGCCATTTTCATGGACTGTGGT 486

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle---------- 81
              ||||||||||||||||||||||||||   |||||||||   ||||||:::
Db        487 TTCCATGCCAGAGAATGGATTTCCCATGCATTTTGCCAGTGGTTTGTGAGAGAGGCTGTT 546

Qy         81 ---------------------------------------------------------- 81

Db        547 CTCACCTATGGATATGAGAGTCACATGACAGAATTCCTCAACAAGCTAGACTTTTATGTC 606

Qy         82 ----------------------GlyHis------------------AsnArgMetTrpArg 88
                                    |||:::                 ||||||||||||||
Db        607 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGA 666

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
              |||   ||||||      |||          ||||||||||||||   ||||||||||||
Db        667 AAGACCCGCTCTACCAATGCTGGAACTACCTGCATTGGCACAGACCCCAACAGAAATTTT 726

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
                  ||||||      |||||||||:::      |||   ||||||||||||
Db        727 ---GATGCTGGGTGGTGCACAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGT 783

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
              |||         |||||||||   |||   ||||||:::|||   |||:::|||   |||
Db        784 GGATCTGCTGCAGAGTCTGAAAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAAC 843

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
              ::::::   ||||||||||||:::::::::|||||||||||||||||   |||::::::|||
Db        844 CTCTCCTCCATCAAAGCATACCTGACGATCCACTCATACTCACAGATGATACTCTACCCT 903

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||                 :::::::::   ||||||:::   :::|||
Db        904 TATTCCTATGATTACAAACTCCCCGAGAACAATGCTGAGTTGAATAACCTGGCTAAGGCT 963

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
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```
                ||||||:::   :::      |||        |||:::||||||:::|||   |||:::
Db        964 GCCGTGAAAGAACTT---GCTACACTGTATGGCACCAAGTACACATACGGCCCAGGAGCT 1020

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
              |||:::|||   |||   ||||||   |||||||||   ||||||   ||||||||||
Db       1021 ACAACAATCTATCCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAA 1080

Qy        229 TyrSerPheThr 232
              |||||||||||
Db       1081 TATTCCTTCACC 1092

RESULT 10
US-08-860-882A-67
; Sequence 67, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  999 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-67

Alignment Scores:
Pred. No.:              3.45e-63      Length:         999
Score:                  567.00        Matches:        111
Percent Similarity:     58.36%        Conservative:   46
Best Local Similarity:  41.26%        Mismatches:     72
Query Match:            42.38%        Indels:         40
DB:                     2             Gaps:           5

US-09-980-881A-4 (1-246) x US-08-860-882A-67 (1-999)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::      ||||||:::|||:::      |||   :::|||   :::
Db         67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 126

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::      :::|||   ::::::::::::      |||||:::::||||||
Db        127 CAAGTCGCCACTGAGAATCCAGCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAG 186

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::||||||||   ||||||           |||   ||||||
Db        187 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        244 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 303

Qy         81 Ile---------------------------------------------------------- 81
              :::
Db        304 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363

Qy         82 ----------------------------------GlyHis------------------ 83
                                                |||:::
Db        364 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||   ||||||||||   ||||||   :::      :::   ||||||||||||||
Db        424 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 483

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||           |||||||||   |||||||||   :::   |||
Db        484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 540

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||          |||||||||   |||   ||||||:::|||
Db        541 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGAT 600

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||      ::::::   ||||||||||:::::::::||||||||||||||||
Db        601 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660

Qy        164 HisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::|||||||||||                :::::::::   ||||||:::
Db        661 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 720

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
                 :::|||         |||:::   :::      :::         |||:::||||||
Db        721 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db        778 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 837

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
              |||   ||||||:::||||||||||||
Db        838 GACCAAGGAATCAGATATTCCTTCACC 864

RESULT 11
US-09-011-769A-50
; Sequence 50, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
```

```
;           ZIP: 20005
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: 1.44 Mb disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/011,769A
;           FILING DATE: 13-Feb-1998
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: PCT/GB96/01975
;           FILING DATE: 13-AUG-1996
;           APPLICATION NUMBER: GB 9612295.7
;           FILING DATE: 12-JUN-1996
;           APPLICATION NUMBER: GB 9611019.2
;           FILING DATE: 25-MAY-1996
;           APPLICATION NUMBER: GB 9516810.0
;           FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 50:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 999 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION: 1..987
;       FEATURE:
;           NAME/KEY:  mat_peptide
;           LOCATION: 67..987
;       SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-011-769A-50

Alignment Scores:
Pred. No.:                3.45e-63        Length:          999
Score:                    567.00          Matches:         111
Percent Similarity:       58.36%          Conservative:    46
Best Local Similarity:    41.26%          Mismatches:      72
Query Match:              42.38%          Indels:          40
DB:                       4               Gaps:            5

US-09-980-881A-4 (1-246) x US-09-011-769A-50 (1-999)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::      ||||||:::|||:::          |||   :::|||    :::
Db         67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 126

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::       :::|||   ::::::::::      ||||||:::::||||||
Db        127 CAAGTCGCCACTGAGAATCCAGCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAG 186

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::|||||||||   ||||||             |||   ||||||
Db        187 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::||||||||   ||||||||||||||||||||||||||||||    ||||||
Db        244 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 303

Qy         81 Ile------------------------------------------------------- 81
              :::
Db        304 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363

Qy         82 ----------------------------------GlyHis------------------ 83
                                                |||:::
Db        364 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||   |||||||||   ||||||   :::      :::   ||||||||||||||
Db        424 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 483

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||          |||||||||   |||||||||   :::   |||
Db        484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 540

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||          |||||||||   |||   |||||:::|||
Db        541 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGAT 600

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||      ::::::   ||||||||||||:::::::::||||||||||||||||
Db        601 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660

Qy        164 HisIleValProProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::||||||||||||          :::::::::   ||||||:::
Db        661 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 720

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::|||          |||:::   :::      :::          |||:::||||||
Db        721 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   ||||||||   |||
Db        778 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 837

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
              |||   ||||||:::||||||||||||
Db        838 GACCAAGGAATCAGATATTCCTTCACC 864

RESULT 12
US-08-860-882A-64
; Sequence 64, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1053 bases
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-64

Alignment Scores:
Pred. No.:                3.76e-63        Length:          1053
Score:                    567.00          Matches:         111
Percent Similarity:       58.36%          Conservative:    46
Best Local Similarity:    41.26%          Mismatches:      72
Query Match:              42.38%          Indels:          40
DB:                       2               Gaps:            5

US-09-980-881A-4 (1-246) x US-08-860-882A-64 (1-1053)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::         ||||||:::|||:::          |||   :::|||    :::
Db         67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 126

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::          :::|||   ::::::::::::      ||||||:::::|||||||
Db        127 CAAGTCGCCACTGAGAATCCAGCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAG 186

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::||||||||||   ||||||              |||   ||||||
Db        187 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::||||||||   ||||||||||||||||||||||||||||||   ||||||
Db        244 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 303

Qy         81 Ile------------------------------------------------------- 81
              :::
Db        304 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363

Qy         82 ----------------------------------GlyHis------------------ 83
                                                  |||:::
Db        364 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||   ||||||||   ||||||   :::      :::   |||||||||||||||
Db        424 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 483

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||          |||||||||   |||||||||   :::   |||
Db        484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 540

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||          |||||||||   |||   ||||||:::|||
Db        541 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGAT 600

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||      ::::::   ||||||||||||:::::::::||||||||||||||
Db        601 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::||||||||||||          :::::::::   ||||||:::
Db        661 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 720

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::|||         |||:::   :::      :::         |||:::||||||
Db        721 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db        778 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 837

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
              |||   |||||||:::||||||||||||
Db        838 GACCAAGGAATCAGATATTCCTTCACC 864

RESULT 13
US-09-011-769A-46
; Sequence 46, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;  INFORMATION FOR SEQ ID NO: 46:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1053 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION: 1..1047
;       FEATURE:
;            NAME/KEY:  mat_peptide
;            LOCATION: 67..1047
;       SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-011-769A-46

Alignment Scores:
Pred. No.:                3.76e-63        Length:          1053
Score:                    567.00          Matches:         111
Percent Similarity:       58.36%          Conservative:    46
Best Local Similarity:    41.26%          Mismatches:      72
Query Match:              42.38%          Indels:          40
DB:                       4               Gaps:            5

US-09-980-881A-4 (1-246) x US-09-011-769A-46 (1-1053)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::         ||||||:::|||:::          |||   :::|||    :::
Db         67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 126

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::          :::|||   ::::::::::::      ||||||:::::|||||||
Db        127 CAAGTCGCCACTGAGAATCCAGCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAG 186

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::||||||||||   ||||||              |||   ||||||
Db        187 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243
```

```
Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::|||||||||  ||||||||||||||||||||||||||||||||  ||||||
Db        244 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 303

Qy         81 Ile---------------------------------------------------------- 81
              :::
Db        304 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363

Qy         82 ----------------------------------GlyHis------------------ 83
                                                |||:::
Db        364 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||  |||||||||  ||||||  :::      :::   ||||||||||||||||
Db        424 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 483

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||            |||||||||  |||||||||   :::   |||
Db        484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 540

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||        |||||||||  |||  ||||||:::|||
Db        541 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGAT 600

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||      ::::::  ||||||||||:::::::|||||||||||||||||
Db        601 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::|||||||||||||                :::::::::   ||||||:::
Db        661 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 720

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::|||        |||:::  :::   :::        |||:::||||||
Db        721 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||  |||:::  |||:::|||  |||  ||||||  |||||||||  |||
Db        778 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 837

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
              |||  ||||||:::||||||||||||
Db        838 GACCAAGGAATCAGATATTCCTTCACC 864

RESULT 14
US-08-860-882A-56
; Sequence 56, Application US/08860882A
; Patent No. 5985281
;  GENERAL INFORMATION:
;    APPLICANT:  TAYLORSON, CHRISTOPHER JOHN
;    APPLICANT:  EGGELTE, HENDRIKUS JOHANNES
;    APPLICANT:  TARRAGONA-FIOL, ANTONIO
;    APPLICANT:  RABIN, BRIAN ROBERT
;    APPLICANT:  BOYLE, FRANCIS THOMAS
;    APPLICANT:  HENNAM,JOHN FREDERICK
;    APPLICANT:  BLAKELY, DAVID CHARLES
;    APPLICANT:  MARSHAM, PETER ROBERT
;    APPLICANT:  HEATON, DAVID WILLIAM
;    APPLICANT:  DAVIES, DAVID HUW
;    TITLE OF INVENTION:  CHEMICAL COMPOUNDS
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,882A
;      FILING DATE:  JUNE 23, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DONALD J. BIRD
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  9901/238653
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3027
;      TELEFAX:  (202) 822-0944
;      TELEX:  6174627 CUSH
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1263 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-860-882A-56

Alignment Scores:
Pred. No.:                5.08e-63        Length:           1263
Score:                    567.00          Matches:          111
Percent Similarity:       58.36%          Conservative:     46
Best Local Similarity:    41.26%          Mismatches:       72
Query Match:              42.38%          Indels:           40
DB:                       2               Gaps:             5

US-09-980-881A-4 (1-246) x US-08-860-882A-56 (1-1263)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrH::sSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::        ||||||:::|||:::          |||   :::|||  :::
Db        325 GCAACAGGACACAGTTATGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 384

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
                 :::        :::|||  ::::::::::::      ||||||:::::||||||
Db        385 CAAGTCGCCACTGAGAATCCAGCCCTCACTCTCTGCAGTGTTATCGGAACCACATTTGAG 444

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::||||||||  ||||||          |||   ||||||
Db        445 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 501

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::|||||||||  ||||||||||||||||||||||||||||||||  ||||||
Db        502 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 561

Qy         81 Ile---------------------------------------------------------- 81
              :::
Db        562 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 621

Qy         82 ----------------------------------GlyHis------------------ 83
                                                |||:::
Db        622 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 681

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||  |||||||||  ||||||  :::      :::   ||||||||||||||||
Db        682 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 741

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||            |||||||||  |||||||||   :::   |||
Db        742 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 798

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||        |||||||||  |||  ||||||:::|||
Db        799 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGAT 858

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||      ::::::  ||||||||||:::::::|||||||||||||||||
Db        859 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 918

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::|||||||||||||                :::::::::   ||||||:::
```

```
Db        919 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 978

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::|||       |||:::   :::     :::       |||:::||||||
Db        979 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 1035

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db       1036 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 1095

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
              |||   ||||||:::|||||||||||
Db       1096 GACCAAGGAATCAGATATTCCTTCACC 1122

RESULT 15
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 38:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1263 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

Alignment Scores:
Pred. No.:              5.08e-63        Length:         1263
Score:                  567.00          Matches:        111
Percent Similarity:     58.36%          Conservative:   46
Best Local Similarity:  41.26%          Mismatches:     72
Query Match:            42.38%          Indels:         40
DB:                     4               Gaps:           5

US-09-980-881A-4 (1-246) x US-09-011-769A-38 (1-1263)
```

```
Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              |||:::         ||||||:::|||:::           |||   :::|||   :::
Db        325 GCAACAGGACACAGTTATGAGAAGTACAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 384

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              :::       :::|||   ::::::::::::      ||||||::::::||||||
Db        385 CAAGTCGCCACTGAGAATCCAGCCCTCATCTCTCGCAGTGTTATCGGAACCACATTTGAG 444

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
                    :::|||:::|||||||||   ||||||          |||   ||||||
Db        445 GGACGCGCTATTTACCTCCTGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 501

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ::::::|||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        502 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCCTGCATTCTGCCAGTGGTTT 561

Qy         81 Ile------------------------------------------------------- 81
              :::
Db        562 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 621

Qy         82 ----------------------------------GlyHis------------------ 83
                                                 |||:::
Db        622 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 681

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              :::|||   |||||||||   ||||||   :::       :::   ||||||||||||||
Db        682 AGCCGATTTTGGAGAAAGACTCGCTCCACCCATACTGGATCTAGCTGCATTGGCACAGAC 741

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
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Db        742 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGT 798

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||          |||||||||   |||   ||||||:::|||
Db        799 GATGAAACTTACTGTGGACCTGCCGCAGAGTCTGAAAAGGAAACCAAGGCCCTGGCTGAT 858

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              |||:::|||       ::::::   ||||||||||||:::::::::||||||||||||||||
Db        859 TTCATCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 918

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              :::::::::|||||||||||||                :::::::::   ||||||:::
Db        919 ATGATGATCTACCCTTACTCATATGCTTACAAACTCGGTGAGAACAATGCTGAGTTGAAT 978

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              :::|||         |||:::   :::     :::         |||:::||||||
Db        979 GCCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 1035

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              :::|||   |||:::   |||:::|||   |||   ||||||   |||||||||   |||
Db       1036 TATGGCCCGGGAGCTACAACAATCTATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 1095

Qy        224 AspLeuGlyIleLysTyrSerPheThr 232
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Db       1096 GACCAAGGAATCAGATATTCCTTCACC 1122


Search completed: October 31, 2004, 04:40:06
Job time : 78.6631 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 428.415 Seconds
(without alignments)
2944.316 Million cell updates/sec

Title: US-09-980-881A-4
Perfect score: 1338
Sequence: 1 ASASYYEQYHSLNEIYSWIE.....IKYSFTSNPPVEKLLPLSLK 246

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1289.5	96.4	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1289.5	96.4	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1272	95.1	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1248.5	93.3	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1248.5	93.3	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1177	88.0	1272	15	US-10-379-836-1	Sequence 1, Appli
7	902	67.4	1400	9	US-09-925-302-24	Sequence 24, Appl
8	902	67.4	1400	10	US-09-925-302-24	Sequence 24, Appl
9	869.5	65.0	1037	16	US-10-115-479-63	Sequence 63, Appl
10	830.5	62.1	1132	16	US-10-115-479-65	Sequence 65, Appl
11	556.5	41.6	1302	17	US-10-477-515-1	Sequence 1, Appli
12	556.5	41.6	1311	13	US-10-200-344-9	Sequence 9, Appli
13	556.5	41.6	1993	15	US-10-274-639-33	Sequence 33, Appl
14	556.5	41.6	1993	16	US-10-333-574-33	Sequence 33, Appl
15	554.5	41.4	1907	18	US-10-757-262-127	Sequence 127, App
16	552	41.3	1254	14	US-10-229-546-3	Sequence 3, Appli
17	552	41.3	1622	14	US-10-229-546-1	Sequence 1, Appli
18	552	41.3	1622	15	US-10-429-802-21	Sequence 21, Appl
19	552	41.3	1622	16	US-10-430-503-12	Sequence 12, Appl
20	552	41.3	1622	16	US-10-262-511-71	Sequence 71, Appl
21	552	41.3	1622	16	US-10-641-643-1020	Sequence 1020, Ap
22	552	41.3	1633	15	US-10-341-434-187	Sequence 187, App
23	552	41.3	1740	14	US-10-116-802-95	Sequence 95, Appl
24	550.5	41.1	1125	9	US-09-888-615-2	Sequence 2, Appli
25	550.5	41.1	1332	15	US-10-176-306-75	Sequence 75, Appl
26	550.5	41.1	1603	15	US-10-176-306-73	Sequence 73, Appl
27	549	41.0	1870	9	US-09-910-059-112	Sequence 112, App
28	549	41.0	1870	17	US-10-608-710-3	Sequence 3, Appli
29	549	41.0	2154	9	US-09-910-059-124	Sequence 124, App
30	547.5	40.9	1332	9	US-09-954-456-1141	Sequence 1141, Ap
31	543.5	40.6	1826	15	US-10-252-157-453	Sequence 453, App
32	533.5	39.9	991	16	US-10-383-201-93	Sequence 93, Appl
33	525.5	39.3	2128	13	US-10-200-344-13	Sequence 13, Appl
34	523.5	39.1	1295	17	US-10-363-829-148	Sequence 148, App
35	492	36.8	1200	14	US-10-200-910-7	Sequence 7, Appli
36	492	36.8	1200	18	US-10-843-130-7	Sequence 7, Appli
37	471.5	35.2	1050	13	US-10-200-344-11	Sequence 11, Appl
38	465.5	34.8	1254	9	US-09-925-297-58	Sequence 58, Appl
39	465.5	34.8	1260	15	US-10-345-680-66	Sequence 66, Appl
40	465.5	34.8	1260	16	US-10-257-174-16	Sequence 16, Appl
41	465.5	34.8	1279	16	US-10-236-417-217	Sequence 217, App
42	465.5	34.8	1290	16	US-10-236-417-219	Sequence 219, App
43	465.5	34.8	1311	14	US-10-200-910-5	Sequence 5, Appli
44	465.5	34.8	1311	16	US-10-257-174-15	Sequence 15, Appl
45	465.5	34.8	1311	17	US-10-451-821-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

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Pred. No.:              1.39e-159       Length:         1625
Score:                  1289.50         Matches:        244
Percent Similarity:     92.42%          Conservative:   0
Best Local Similarity:  92.42%          Mismatches:     2
Query Match:            96.38%          Indels:         18
DB:                     9               Gaps:           1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 418

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 478

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        479 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATA 538

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 598

Qy         81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATC 658

Qy        101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGT 718

Qy        121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 TCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCA 778

Qy        141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
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Db        779 GTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCA 838

Qy        161 TyrSerGlnHisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 TACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAG 898

Qy        181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        899 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACC 958

Qy        201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGAT 1018

Qy        221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe--------------------------- 231
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Db       1019 TGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACA 1078

Qy        232 -------------------------ThrSerAsnProProValGluLysLeuLeuProLe 243
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Db       1079 TACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCT 1138

Qy        243 uSerLeuLys 246
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Db       1139 GTCTCTAAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001173DIV
;  CURRENT APPLICATION NUMBER: US/10/212,877
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: 09/813,133
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores:
Pred. No.:              1.39e-159       Length:         1625
Score:                  1289.50         Matches:        244
Percent Similarity:     92.42%          Conservative:   0
Best Local Similarity:  92.42%          Mismatches:     2
Query Match:            96.38%          Indels:         18
DB:                     14              Gaps:           1

US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 418

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 478

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        479 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATA 538

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
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Db        539 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 598

Qy         81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATC 658

Qy        101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
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Db        659 GGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGT 718

Qy        121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
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Db        719 TCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCA 778

Qy        141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
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Db        779 GTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCA 838

Qy        161 TyrSerGlnHisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
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Db        839 TACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAG 898

Qy        181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        899 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACC 958

Qy        201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
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Db        959 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGAT 1018

Qy        221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe--------------------------- 231
              |||||||||||||||||||||||||||||||
Db       1019 TGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACA 1078

Qy        232 -------------------------ThrSerAsnProProValGluLysLeuLeuProLe 243
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Db       1079 TACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCT 1138

Qy        243 uSerLeuLys 246
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Db       1139 GTCTCTAAAA 1148

RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
;   LENGTH: 1728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

Alignment Scores:
Pred. No.:             3.17e-157     Length:         1728
Score:                 1272.00       Matches:        246
Percent Similarity:    81.73%        Conservative:   0
Best Local Similarity: 81.73%        Mismatches:     0
Query Match:           95.07%        Indels:         55
DB:                    9             Gaps:           2

US-09-980-881A-4 (1-246) x US-09-880-107-2396 (1-1728)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
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Db        362 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 421

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 481

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATA 541

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCTTTCTGCTTGTGGTTC 601

Qy         81 IleGlyHis--------------------------------------------------- 83
              |||||||||
Db        602 ATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTT 661

Qy         83 ------------------------------------------------------------ 83

Db        662 GTGGATTTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 721

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGAC 781

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 CTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 841

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGT 901

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 TTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAG 961

Qy        164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 CATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCT 1021

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACA 1081

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTAT 1141

Qy        224 AspLeuGlyIleLysTyrSerPhe------------------------------------ 231
              ||||||||||||||||||||||||
Db       1142 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTC 1201

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                              ||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAA 1261

Qy        246 s 246
              |
Db       1262 A 1262

RESULT 4
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
```

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;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.:              2.71e-154      Length:          1344
Score:                  1248.50        Matches:         244
Percent Similarity:     79.74%         Conservative:    0
Best Local Similarity:  79.74%         Mismatches:      2
Query Match:            93.31%         Indels:          60
DB:                     16             Gaps:            3

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 432

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 492

Qy         41 LysTyrProLeuTyrValLeuLys--------------ValSerGlyLysGluGlnThr 55
              ||||||||||||||||||||||||              ||||||||||||||||||
Db        493 AAGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCA 552

Qy         56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCT 612

Qy         76 PheCysLeuTrpPheIleGlyHis---------------------------------- 83
              ||||||||||||||||||||||||
Db        613 TTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACC 672

Qy         83 ---------------------------------------------------------- 83

Db        673 AATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGAC 732

Qy         84 --------------AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
                           ||||||||||||||||||||||||||||||||||||||||||||
Db        733 TACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCAT 792

Qy         99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 TGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCA 852

Qy        119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        853 TCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTG 912

Qy        139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATG 972

Qy        159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 CATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGAC 1032

Qy        179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAA 1092

Qy        199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 AATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGG 1152

Qy        219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe---------------------- 231
              ||||||||||||||||||||||||||||||||||||||
Db       1153 GACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACG 1212

Qy        232 -------------------------------ThrSerAsnProProValGluLysLeuLe 241
                                            ||||||||||||||||||||||||||||||
Db       1213 GGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTT 1272

Qy        241 uProLeuSerLeuLys 246
              ||||||||||||||||
Db       1273 GCCGCTGTCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
```

```
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:
Pred. No.:              4.12e-154       Length:         1743
Score:                  1248.50         Matches:        244
Percent Similarity:     79.74%          Conservative:   0
Best Local Similarity:  79.74%          Mismatches:     2
Query Match:            93.31%          Indels:         60
DB:                     16              Gaps:           3

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 421

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 481

Qy         41 LysTyrProLeuTyrValLeuLys----------------ValSerGlyLysGluGlnThr 55
              ||||||||||||||||||||||||                ||||||||||||||||||
Db        482 AAGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCA 541

Qy         56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCT 601

Qy         76 PheCysLeuTrpPheIleGlyHis----------------------------------- 83
              |||||||||||||||||||||||
Db        602 TTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACC 661

Qy         83 ------------------------------------------------------------ 83

Db        662 AATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCAGTGGTTAATGTGGATGGTTATGAC 721

Qy         84 ---------------AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
                            ||||||||||||||||||||||||||||||||||||||||||||
Db        722 TACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCAT 781

Qy         99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 TGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCA 841

Qy        119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGTG 901

Qy        139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AAGGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATG 961

Qy        159 HisSerTyrSerGlnHisIleValProTyrSerTyrThrArgSerLysSerLysAsp 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 CATTCATACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGAC 1021

Qy        179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 CATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAA 1081

Qy        199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGG 1141

Qy        219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe--------------------- 231
              |||||||||||||||||||||||||||||||||||||||
Db       1142 GACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACG 1201

Qy        232 ------------------------------ThrSerAsnProProValGluLysLeuLe 241
                                             ||||||||||||||||||||||||||||||
Db       1202 GGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTT 1261

Qy        241 uProLeuSerLeuLys 246
              ||||||||||||||||
Db       1262 GCCGCTGTCTCTAAAA 1277

RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
;  TITLE OF INVENTION:  TAFI
;  FILE REFERENCE: D0214NP
;  CURRENT APPLICATION NUMBER: US/10/379,836
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: U.S. 60/361,523
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Papio hamadryas
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1269)
US-10-379-836-1

Alignment Scores:
Pred. No.:              7.14e-145       Length:         1272
Score:                  1177.00         Matches:        228
Percent Similarity:     78.41%          Conservative:   8
Best Local Similarity:  75.75%          Mismatches:     10
Query Match:            87.97%          Indels:         55
DB:                     15              Gaps:           2

US-09-980-881A-4 (1-246) x US-10-379-836-1 (1-1272)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 402

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              |||||||||:::::|||||||||||||||||||||||||||||||||||:::|||
Db        403 CTTATAACTGAGAAGTATCCTGATATGCTTACAAAAATCCACATTGGATCCTCCTATGAG 462

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||:::
Db        463 AAGCACCCACTTTATGTTTTAAAGGTTTCTGGAAAAGAACAAACAGCCAAAAATGCCATG 522

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        523 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCCCCTGCTTTCTGCTTGTGGTTC 582

Qy         81 IleGlyHis---------------------------------------------------- 83
              |||||||||
Db        583 ATAGGCCATATAACTGAATACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCAT 642

Qy         83 ---------------------------------------------------------- 83

Db        643 GTGGATTTCTATGTTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAG 702

Qy         84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCGTTGCATCGGAACAGAC 762

Qy        104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGAACAGGAACTTTGCGTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGC 822

Qy        124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        823 TCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCAGAAGCGAAGGCGGTGGCTAAT 882

Qy        144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 TTCTTGAGAAGAAATATCAACCACATTAAAGCATACATCAGCATGCATTCATACTCCCAG 942

Qy        164 HisIleValProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CATATCGTGTTTCCATATTCCTATACTCGAAGCAAAAGCAAAGACCACGAGGAATTGTCT 1002

Qy        184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
              ||||||||||||||||||||||||||||||:::||||||||||||||||   |||||||||
Db       1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTCAGAAAACCAGTAAAAATATCAGGTATACA 1062

Qy        204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
              ||||||   ||||||||||||||||||||||||||||||||   ||||||||||||||||
Db       1063 CATGGCCGTGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGCGGACGATTGGATCTAT 1122

Qy        224 AspLeuGlyIleLysTyrSerPhe------------------------------------ 231
              |||||||||||||||||||||||
Db       1123 GATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCAAATACGGATTC 1182

Qy        232 ----------------ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLy 246
                             ||||||||||||   |||:::   ||||||||||||||||||||
Db       1183 TTGCTGCCTGAGCGTTACATCAAACCCACTTGTAAAGACGCTTTTGCCGCTGTCTCTAAA 1242

Qy        246 s 246
              |
Db       1243 A 1243

RESULT 7
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.:              1.99e-108      Length:          1400
Score:                  902.00         Matches:         181
Percent Similarity:     76.05%         Conservative:    0
Best Local Similarity:  76.05%         Mismatches:      1
Query Match:            67.41%         Indels:          56
DB:                     9              Gaps:            2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy         65 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy         83 ---------------------------------------------------------- 83

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy         84 ----------------------------------------------------AsnArgMetTr 87
                                                                  ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189

Qy         87 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        127 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        147 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 167
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        167 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 207
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 227
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        227 eLysTyrSerPhe------------------------------------------------ 231
              |||||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
                   ||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 719

RESULT 8
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
```

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;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.:              1.99e-108      Length:          1400
Score:                  902.00         Matches:         181
Percent Similarity:     76.05%         Conservative:    0
Best Local Similarity:  76.05%         Mismatches:      1
Query Match:            67.41%         Indels:          56
DB:                     10             Gaps:            2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy         65 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         10 GGAATCCATGCCAGANAATGGATCTCTCCTGCTTTCTGCTTGTGGTTCATAGGCCATATA 69

Qy         83 ------------------------------------------------------------ 83

Db         70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTAT 129

Qy         84 ----------------------------------------------AsnArgMetTr 87
                                                              ||||||||||
Db        130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACTACTCATGGAAAAAGAATCGAATGTG 189

Qy         87 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GAGAAAGAACCGTTCTTTCTATGCGAACAATCATTGCATCGGAACAGACCTGAATAGGAA 249

Qy        107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309

Qy        127 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCAGTGGCTAGTTTCTTGAGAAG 369

Qy        147 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAATATCAACCAGATTAAAGCATACATCAGCATGCATTCATACTCCCAGCATATAGTGTT 429

Qy        167 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAGGAACTGTCTCTAGTAGCCAG 489

Qy        187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACACATGGCCATGG 549

Qy        207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGATTGGATCTATGATTTGGGCAT 609

Qy        227 eLysTyrSerPhe---------------------------------------------- 231
              |||||||||||
Db        610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTGCCGGA 669

Qy        232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
                   ||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 719

RESULT 9

US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.:              2.45e-104      Length:          1037
Score:                  869.50         Matches:         180
Percent Similarity:     68.18%         Conservative:    0
Best Local Similarity:  68.18%         Mismatches:      2
Query Match:            64.99%         Indels:          82
DB:                     16             Gaps:            2
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US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 442

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTGAG 502

Qy         41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        503 AAGTACCCACTCTATGTTTTAAAGGTTTCTGGAAAAGAACAAGCAGCCAAAAATGCCATA 562

Qy         61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
              ||||||||
Db        563 TGGATTGAC---------------------------------------------------- 571

Qy         81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100

Db        571 ---------------------------------------------------------- 571

Qy        101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120

Db        571 ---------------------------------------------------------- 571

Qy        121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
                                  ||||||||||||||||||||||||||||||||||||||
Db        572 --------------------TGTGGACTTTATCCTGAGTCAGAACCAGAAGTGAAGGCA 610

Qy        141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTCA 670

Qy        161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 TACTCCCAGCATATAGTGTTTCCATATTCCTATACACGAAGTAAAAGCAAAGACCATGAG 730

Qy        181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        731 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACC 790

Qy        201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGGACGAT 850

Qy        221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe--------------------------- 231
              |||||||||||||||||||||||||||||||
Db        851 TGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACA 910

Qy        232 -------------------------ThrSerAsnProProValGluLysLeuLeuProLe 243
                                        ||||||||||||||||||||||||||||||||||
Db        911 TACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTGCCGCT 970

Qy        243 uSerLeuLys 246
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Db        971 GTCTCTAAAA 980
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RESULT 10
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Smithson, Glendda
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Boldog, Ferenc L.;
;  APPLICANT:  Voss, Edward
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  MacDougall, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Malyanker, Uriel M.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-322 B (Cura 622 PT)
;  CURRENT APPLICATION NUMBER: US/10/115,479
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,657
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,678
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,687
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: 60/285,325
;  PRIOR FILING DATE: 2001-04-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
;   LENGTH: 1132
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.:                4.07e-99        Length:          1132
Score:                    830.50          Matches:         171
Percent Similarity:       55.88%          Conservative:    0
Best Local Similarity:    55.88%          Mismatches:      1
Query Match:              62.07%          Indels:          134
DB:                       16              Gaps:            4

US-09-980-881A-4 (1-246) x US-10-115-479-65 (1-1132)

Qy          1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAA 442

Qy         21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGGATCCTCATTTGAG 502

Qy         41 LysTyrProLeuTyrValLeuLys----------------ValSerGlyLysGluGlnThr 55
              ||||||||||||||||||||||||                ||||||||||||||||||
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```
Db        503 AAGTACCCACTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAGAACAAGCA 562

Qy         56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla  75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 GCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCCTGCT 622

Qy         76 PheCysLeuTrpPheIleGlyHis---------------------------------- 83
              ||||||||||||||||||||||||
Db        623 TTCTGCTTGTGGTTCATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACC 682

Qy         83 ------------------------------------------------------------ 83

Db        683 AATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGAC 742

Qy         84 --------------AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis  98
                           ||||||||||||||||||||||||||||||||||||||||||||||
Db        743 TACTCATGGAAAAAGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCAT 802

Qy         99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCA 862

Qy        119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 TCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAG--------------- 907

Qy        139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158

Db        907 ------------------------------------------------------------ 907

Qy        159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178

Db        907 ------------------------------------------------------------ 907

Qy        179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198

Db        907 ------------------------------------------------------------ 907

Qy        199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
                                      ||||||||||||||||||||||||||||||||
Db        908 ------------------------TCAGAAACCTTATACCTAGCTCCTGGAGGTGGG 940

Qy        219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe--------------------- 231
              ||||||||||||||||||||||||||||||||||||||
Db        941 GACGATTGGATCTATGATTTGGGCATCAAATATTCGTTTACAATTGAACTTCGAGATACG 1000

Qy        232 ------------------------------ThrSerAsnProProValGluLysLeuLe 241
                                           ||||||||||||||||||||||||||||||
Db       1001 GGCACATACGGATTCTTGCTGCCGGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTT 1060

Qy        241 uProLeuSerLeuLys 246
              ||||||||||||||||
Db       1061 GCCGCTGTCTCTAAAA 1076

RESULT 11
US-10-477-515-1
; Sequence 1, Application US/10477515
; Publication No. US20040136976A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer AG
;  TITLE OF INVENTION: REGULATION OF HUMAN ZINC CARBOXYPEPTIDASE B-LIKE PROTEIN
;  FILE REFERENCE: LIO355 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/477,515
;  CURRENT FILING DATE:  2003-11-19
;  PRIOR APPLICATION NUMBER: US 60/292,329
;  PRIOR FILING DATE: 2001-05-22
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-477-515-1

Alignment Scores:
Pred. No.:                8.98e-63        Length:          1302
Score:                    556.50          Matches:         113
Percent Similarity:       53.45%          Conservative:    42
Best Local Similarity:    38.97%          Mismatches:      77
Query Match:              41.59%          Indels:          58
DB:                       17              Gaps:            5

US-09-980-881A-4 (1-246) x US-10-477-515-1 (1-1302)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||   ||||||||||||   ||||||   :::|||:::      :::   :::
Db        406 TATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT 465

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              |||      ::::::            ||||||   |||:::|||          |||:::
Db        466 CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTTT 525

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::||||||:::   |||:::            |||   |||:::|||||||||||||||
Db        526 ATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGGT 582

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81
              ||||||||||||||||||||   ||||||||||||   ||||||:::
Db        583 ATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTT 642

Qy         81 ------------------------------------------------------------ 81

Db        643 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702

Qy         82 ----------------------------------------GlyHisAsnArgMetTrpArg  88
                                                      :::::::|||   ||||||
Db        703 ATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 762

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
              |||   ||||||      :::         |||   |||   |||   |||||||||:::
Db        763 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 822

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
              |||   ||||||:::||||||||||||          |||   :::||||||||||
Db        823 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATACTGT 879

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
              |||   :::||||||||||||||||||||||||||||||:::|||||||||::::::
Db        880 GGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAACAC 939

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
                  |||:::||||||:::|||   |||:::|||:::|||   ::::::::::|||
Db        940 AGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTATCCC 999

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||      :::         :::         :::         |||   :::
Db       1000 TATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1059

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
              ||||||   |||::::::                  ||||||   :::|||      |||
Db       1060 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCCTCC 1116

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
                 |||||||||::::::   |||          ||||||   |||      ||||||
Db       1117 ACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATACCT 1176

Qy        229 TyrSerPhe---------------------------------------------------- 231
              |||:::|||
Db       1177 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAGATG 1236

Qy        232 -ThrSerAsnProProValGluLysLeu 240
               :::||||||||||||||:::||||||
Db       1237 CTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 12
US-10-200-344-9
```

```
; Sequence 9, Application US/10200344
; Publication No. US20020173641A1
; GENERAL INFORMATION:
;  APPLICANT: Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020173641A1el Human Carboxypeptidases and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0047-USA
;  CURRENT APPLICATION NUMBER: US/10/200,344
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: US/09/675,305
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1311
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.:              9.08e-63      Length:          1311
Score:                  556.50        Matches:         113
Percent Similarity:     53.45%        Conservative:    42
Best Local Similarity:  38.97%        Mismatches:      77
Query Match:            41.59%        Indels:          58
DB:                     13            Gaps:            5

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||  ||||||||||||  ||||||  :::|||:::      :::   :::
Db        406 TATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT 465

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              |||      ::::::            ||||||  |||:::|||          |||:::
Db        466 CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTTT 525

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::||||||:::   |||:::            |||   |||:::||||||||||||||||
Db        526 ATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGGT 582

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81
              ||||||||||||||||||  ||||||||||||  ||||||:::
Db        583 ATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTT 642

Qy         81 ------------------------------------------------------------ 81

Db        643 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702

Qy         82 -------------------------------------GlyHisAsnArgMetTrpArg 88
                                                  ::::::|||   ||||||
Db        703 ATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 762

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
              |||   ||||||      :::          |||   |||   |||   |||||||||:::
Db        763 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 822

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
                  |||   ||||||:::|||||||||||||          |||   :::|||||||||
Db        823 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATACTGT 879

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
              |||   :::||||||||||||||||||||||||||||||:::|||||||||::::::
Db        880 GGCCCTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAACAC 939

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
                  |||:::||||||:::|||   |||:::|||:::|||   ::::::::::|||
Db        940 AGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTATCCC 999

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||      :::      :::      :::      |||      :::
Db       1000 TATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1059

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
              ||||||   |||::::::                  ||||||   :::|||      |||
Db       1060 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCCTCC 1116

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
                  |||||||||::::::   |||      ||||||   |||      ||||||
Db       1117 ACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATACCT 1176

Qy        229 TyrSerPhe------------------------------------------------------ 231
              |||:::|||
Db       1177 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAGATG 1236

Qy        232 -ThrSerAsnProProValGluLysLeu 240
               :::||||||||||||||||:::||||||
Db       1237 CTCATCAAACCCACCTGTACAGAAACTA 1264

RESULT 13
US-10-274-639-33
; Sequence 33, Application US/10274639
; Publication No. US20030232349A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  DELEGEANE, Angelo M.; GANDHI, Ameena R.
;  APPLICANT:  HAFALIA, April J.A.; LU, Dyung Aina M.
;  APPLICANT:  PATTERSON, Chandra; TRIBOULEY, Catherine M.
;  APPLICANT:  DAS, Debopriya; KALLICK, Deborah A.
;  APPLICANT:  NGUYEN, Danniel B.; LEE, Ernestine A.
;  APPLICANT:  KHAN, Farrah A.; YUE, Henry
;  APPLICANT:  AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
;  APPLICANT:  POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi
;  APPLICANT:  YANG, Junming; THANGAVELU, Kavitha
;  APPLICANT:  DING, Li; KEARNEY, Liam
;  APPLICANT:  BAUGHN, Mariah R.; BOROWSKY, Mark L.
;  APPLICANT:  SANJANWALA, Madhusudan M.; YAO, Monique G.
;  APPLICANT:  BURFORD, Neil; WALIA, Narinder K.
;  APPLICANT:  LAL, Preeti G.; LEE, Sally
;  APPLICANT:  TODD, Stephen; LO, Terence P.
;  APPLICANT:  TANG, Y. Tom; ELLIOTT, Vicki S.
;  APPLICANT:  AZIMZAI, Yalda; LU, Yan
;  TITLE OF INVENTION: PROTEASES
;  FILE REFERENCE: PI-0167 USA
;  CURRENT APPLICATION NUMBER: US/10/274,639
;  CURRENT FILING DATE:  2002-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/22397
;  PRIOR FILING DATE: 2001-07-17
;  PRIOR APPLICATION NUMBER: US 60/220,063
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/221,680
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/223,544
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: US 60/224,717
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: US 60/225,988
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: US 60/227,568
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 33
;   LENGTH: 1993
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030232349A1 4948403CB1
US-10-274-639-33
```

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Alignment Scores:
Pred. No.:                1.78e-62        Length:         1993
Score:                    556.50          Matches:        113
Percent Similarity:       53.45%          Conservative:   42
Best Local Similarity:    38.97%          Mismatches:     77
Query Match:              41.59%          Indels:         58
DB:                       15              Gaps:           5

US-09-980-881A-4 (1-246) x US-10-274-639-33 (1-1993)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||   ||||||||||||   ||||||   :::|||:::      :::   :::
Db        743 TATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT 802

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              |||     ::::::          ||||||   |||:::|||         |||:::
Db        803 CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTTT 862

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::|||||:::   |||:::           |||   |||:::|||||||||||||||
Db        863 ATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGGT 919

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81
              ||||||||||||||||||||   ||||||||||||   ||||||:::
Db        920 ATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTT 979

Qy         81 ------------------------------------------------------------ 81

Db        980 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 1039

Qy         82 ---------------------------------------GlyHisAsnArgMetTrpArg 88
                                                     :::::|||   ||||||
Db       1040 ATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 1099

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
              |||   ||||||      :::         |||   |||   |||   ||||||||:::
Db       1100 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 1159

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
                 |||   ||||||:::||||||||||||         |||   :::||||||||||
Db       1160 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATACTGT 1216

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
              |||   :::||||||||||||||||||||||||||||||:::|||||||:::::
Db       1217 GGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAACAC 1276

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
                   |||:::||||||:::|||   |||:::|||:::|||   :::::::::|||
Db       1277 AGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTATCCC 1336

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||      :::         :::         :::         |||   :::
Db       1337 TATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1396

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
              ||||||   |||::::::                  ||||||   :::|||      |||
Db       1397 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCCTCC 1453

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
                 ||||||||::::::   |||         ||||||   |||         ||||||
Db       1454 ACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATACCT 1513

Qy        229 TyrSerPhe---------------------------------------------------- 231
              |||:::|||
Db       1514 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAGATG 1573

Qy        232 -ThrSerAsnProProValGluLysLeu 240
               :::|||||||||||||||:::|||||||
Db       1574 CTCATCAAACCCACCTGTACAGAAACTA 1601

RESULT 14
US-10-333-574-33
; Sequence 33, Application US/10333574
; Publication No. US20040091962A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  DELEGEANE, Angelo M.; GANDHI, Ameena R.
;  APPLICANT:  HAFALIA, April J.A.; LU, Dyung Aina M.
;  APPLICANT:  ARVIZU, Chandra S.; TRIBOULEY, Catherine M.
;  APPLICANT:  DAS, Debopriya; KALLICK, Deborah A.
;  APPLICANT:  NGUYEN, Danniel B.; LEE, Ernestine A.
;  APPLICANT:  KHAN, Farrah A.; YUE, Henry
;  APPLICANT:  AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
;  APPLICANT:  POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi
;  APPLICANT:  YANG, Junming; THANGAVELU, Kavitha
;  APPLICANT:  DING, Li; KEARNEY, Liam
;  APPLICANT:  BAUGHN, Mariah R.; BOROWSKY, Mark L.
;  APPLICANT:  SANJANWALA, Madhusudan M.; YAO, Monique G.
;  APPLICANT:  BURFORD, Neil; CHAWLA, Narinder K.
;  APPLICANT:  LAL, Preeti G.; LEE, Sally
;  APPLICANT:  TODD, Stephen; LO, Terence P.
;  APPLICANT:  TANG, Y. Tom; ELLIOTT, Vicki S.
;  APPLICANT:  AZIMZAI, Yalda; LU, Yan
;  TITLE OF INVENTION: PROTEASES
;  FILE REFERENCE: PI-0167 USN
;  CURRENT APPLICATION NUMBER: US/10/333,574
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US 01/22397
;  PRIOR FILING DATE: 2001-07-17
;  PRIOR APPLICATION NUMBER: US 60/220,063
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/221,680
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/223,544
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: US 60/224,717
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: US 60/225,988
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: US 60/227,568
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 33
;   LENGTH: 1993
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 4948403CB1
US-10-333-574-33

Alignment Scores:
Pred. No.:                1.78e-62        Length:         1993
Score:                    556.50          Matches:        113
Percent Similarity:       53.45%          Conservative:   42
Best Local Similarity:    38.97%          Mismatches:     77
Query Match:              41.59%          Indels:         58
DB:                       16              Gaps:           5

US-09-980-881A-4 (1-246) x US-10-333-574-33 (1-1993)

Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
              ||||||   ||||||||||||   ||||||   :::|||:::      :::   :::
Db        743 TATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT 802

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
              |||     ::::::          ||||||   |||:::|||         |||:::
Db        803 CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTTT 862

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
              :::|||||:::   |||:::           |||   |||:::|||||||||||||||
Db        863 ATTTTAAAGCTG---GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGGT 919

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81
              ||||||||||||||||||||   ||||||||||||   ||||||:::
```

```
Db        920 ATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTT 979

Qy         81 ------------------------------------------------------------ 81

Db        980 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 1039

Qy         82 ---------------------------------------GlyHisAsnArgMetTrpArg 88

Db       1040 ATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 1099

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108

Db       1100 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 1159

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128

Db       1160 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATACTGT 1216

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148

Db       1217 GGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAACAC 1276

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168

Db       1277 AGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTATCCC 1336

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188

Db       1337 TATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1396

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208

Db       1397 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCCTCC 1453

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228

Db       1454 ACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATACCT 1513

Qy        229 TyrSerPhe---------------------------------------------------- 231

Db       1514 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAGATG 1573

Qy        232 -ThrSerAsnProProValGluLysLeu 240

Db       1574 CTCATCAAACCCACCTGTACAGAAACTA 1601
```

RESULT 15
US-10-757-262-127
; Sequence 127, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (217)...(1530)
US-10-757-262-127

Alignment Scores:

Pred. No.:	3.05e-62	Length:	1907
Score:	554.50	Matches:	113
Percent Similarity:	53.45%	Conservative:	42
Best Local Similarity:	38.97%	Mismatches:	77
Query Match:	41.44%	Indels:	58
DB:	18	Gaps:	5

US-09-980-881A-4 (1-246) x US-10-757-262-127 (1-1907)

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Qy          6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25

Db        622 TATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT 681

Qy         26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45

Db        682 CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATGTCTTTTT 741

Qy         46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65

Db        742 ATTTTAAAGCTG---GGCAGACGATCACCACTCAAAAGAGCTGTTTGGATAGACTGTGGT 798

Qy         66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle------------ 81

Db        799 ATTCATGCAAGAGAATGGATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTT 858

Qy         81 ------------------------------------------------------------ 81

Db        859 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 918

Qy         82 ---------------------------------------GlyHisAsnArgMetTrpArg 88

Db        919 ATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 978

Qy         89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108

Db        979 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 1038

Qy        109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128

Db       1039 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCTTGTGATGACACATACTGT 1095

Qy        129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148

Db       1096 GGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTAGCTAACTTCCTTCGAAAACAC 1155

Qy        149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
```

```
Db       1156 AGAAAGCACATTAGGGCTTATCTCTCCTTTCATGCATATGCTCAGATGTTACTGTATCCC 1215

Qy        169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
              |||||||||       :::         :::         :::         |||   :::
Db       1216 TATTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1275

Qy        189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
              ||||||   |||::::::                  ||||||   :::|||       |||
Db       1276 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCCTCC 1332

Qy        209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
                |||||||||::::::   |||         ||||||   |||      ||||||
Db       1333 ACAACGTTGTATGTGAGCTCTGGTAGCTCAATGGATTGGGCCTACAAAAATGGAATACCT 1392

Qy        229 TyrSerPhe---------------------------------------------------- 231
              |||:::|||
Db       1393 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTTACTCCCAGAGATG 1452

Qy        232 -ThrSerAsnProProValGluLysLeu 240
               :::|||||||||||||||:::||||||
Db       1453 CTCATCAAACCCACCTGTACAGAAACTA 1480
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Search completed: October 31, 2004, 08:40:47
Job time : 436.415 secs

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